

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:40:57 ; Search time 26.7671 Seconds
(without alignments)
1690.542 Million cell updates/sec

Title: US-10-624-932-2_COPY_232_348
Perfect score: 682
Sequence: 1 SASAAVIVYVNGGWSTWTEW.....NGGEECQGTDLDTNRCTSDL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				ID	Description
No.	Score	Match	Length	DB			
1	682	100.0	330	8	ADH71620	ADH71620	Human pro
2	682	100.0	336	8	ADH71614	ADH71614	Human pro
3	682	100.0	898	5	AAU85403	AAU85403	Human pro
4	682	100.0	898	5	AAU97899	AAU97899	Human net
5	682	100.0	898	8	ADH71618	ADH71618	Human pro
6	661	96.9	898	2	AAW78898	AAW78898	Rat UNC-5
7	661	96.9	898	5	AAU10543	AAU10543	Rat netri
8	661	96.9	898	5	AAU97900	AAU97900	Rat netri
9	661	96.9	898	7	ADG42580	ADG42580	Rat trans

10	657.5	96.4	943	4	AAM79128	Aam79128	Human	pro
11	622.5	91.3	331	8	ADH71612	Adh71612	Human	pro
12	622.5	91.3	898	8	ADH71626	Adh71626	Human	pro
13	622.5	91.3	899	5	AAU79939	Aau79939	Human	UNC
14	622.5	91.3	899	7	ADG42569	Adg42569	Novel	hum
15	622.5	91.3	899	8	ADH71636	Adh71636	Human	pro
16	622.5	91.3	899	8	ADH71642	Adh71642	Human	pro
17	622.5	91.3	899	8	ADH71648	Adh71648	Human	pro
18	622.5	91.3	899	8	ADH71632	Adh71632	Human	pro
19	622.5	91.3	899	8	ADH71610	Adh71610	Human	pro
20	622.5	91.3	899	8	ADH71628	Adh71628	Human	pro
21	622.5	91.3	899	8	ADH71640	Adh71640	Human	pro
22	622.5	91.3	899	8	ADH71630	Adh71630	Human	pro
23	622.5	91.3	899	8	ADH71650	Adh71650	Human	pro
24	622.5	91.3	899	8	ADH71644	Adh71644	Human	pro
25	622.5	91.3	899	8	ADH71634	Adh71634	Human	pro
26	622.5	91.3	899	8	ADH71646	Adh71646	Human	pro
27	622.5	91.3	899	8	ADH71638	Adh71638	Human	pro
28	539	79.0	636	8	ADR99262	Adr99262	Splice	va
29	539	79.0	669	8	ADR99252	Adr99252	Human	sRO
30	539	79.0	929	7	ADG42583	Adg42583	Human	tra
31	539	79.0	931	4	AAB50691	Aab50691	Human	UNC
32	539	79.0	931	7	ADE63098	Ade63098	Human	Pro
33	539	79.0	931	7	ADG42584	Adg42584	Human	tra
34	539	79.0	931	7	ABU64297	Abu64297	Human	thr
35	539	79.0	931	8	ADR99258	Adr99258	Human	unc
36	539	79.0	964	8	ADR99250	Adr99250	Human	lRO
37	539	79.0	982	4	ABG11551	Abg11551	Novel	hum
38	531	77.9	931	7	ADG42582	Adg42582	Mouse	tra
39	523	76.7	933	5	AAO18734	Aao18734	Human	NOV
40	523	76.7	933	5	AAO18735	Aao18735	Human	NOV
41	523	76.7	945	4	AAU12244	Aau12244	Human	PRO
42	523	76.7	945	5	ABB09520	Abb09520	Human	tra
43	523	76.7	945	6	ABO17688	AbO17688	Novel	hum
44	523	76.7	945	6	ABU80942	Abu80942	Human	PRO
45	523	76.7	945	6	ABU66642	Abu66642	Human	PRO

ALIGNMENTS

RESULT 1

ADH71620

ID ADH71620 standard; protein; 330 AA.

XX

AC ADH71620;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21f SEQ ID NO:516.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

KW dyslipidaemia.

XX

OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.

PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71619.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 516; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The

PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

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PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71613.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 510; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention..

XX

SQ Sequence 336 AA;

Query Match 100.0%; Score 682; DB 8; Length 336;

Best Local Similarity 100.0%; Pred. No. 1.8e-52;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTAC 60

|||||

Db 210 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTAC 269

Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDL DTRNCTSDL 117
|||||
Db 270 ATLCPVDGSWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDL DTRNCTSDL 326

RESULT 3

AAU85403

ID AAU85403 standard; protein; 898 AA.

XX

AC AAU85403;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human protein NOV1.

XX

KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;

KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;

KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;

KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;

KW psychosis; neurological disorder; anxiety; schizophrenia;

KW manic depression; dementia; dyskinesia; Huntington's disease;

KW Gilles de la Tourette's syndrome; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200210216-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US024225.

XX

PR 28-JUL-2000; 2000US-0221409P.

PR 04-AUG-2000; 2000US-0222840P.

PR 04-AUG-2000; 2000US-0223752P.

PR 04-AUG-2000; 2000US-0223762P.

PR 04-AUG-2000; 2000US-0223769P.

PR 04-AUG-2000; 2000US-0223770P.

PR 14-AUG-2000; 2000US-0225146P.

PR 15-AUG-2000; 2000US-0225392P.

PR 15-AUG-2000; 2000US-0225470P.

PR 16-AUG-2000; 2000US-0225697P.

PR 01-FEB-2001; 2001US-0263662P.

PR 05-APR-2001; 2001US-0281645P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;

PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;

XX

DR WPI; 2002-180074/23.

DR N-PSDB; ABK37922.

XX

PT New isolated cytoplasmic, nuclear, membrane bound, or secreted

PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,

PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.

XX

PS Claim 1; Page 11; 213pp; English.

XX

CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence represents a
CC NOVX protein

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 682; DB 5; Length 898;

Best Local Similarity 100.0%; Pred. No. 5e-52;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTAC 60
|
Db 232 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTAC 291

Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDRNCTSDL 117
|
Db 292 ATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDRNCTSDL 348

RESULT 4

AAU97899

ID AAU97899 standard; protein; 898 AA.

XX

AC AAU97899;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human netrin binding membrane receptor UNC5H-1 protein.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; human; nootropic;
KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
KW central nervous system; CNS; stroke; Parkinson's disease;

KW multiple sclerosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 152. .223

FT /note= "Immunoglobulin domain "

FT Domain 247. .294

FT /note= "Thrombospondine type 1 domain "

FT Domain 302. .348

FT /note= "Thrombospondine type 1 domain"

FT Region 361. .382

FT /note= "Transmembrane region"

FT Domain 495. .598

FT /note= "ZU5 domain"

FT Domain 817. .897

FT /note= "Death domain"

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.

XX

PA (FARB) BAYER AG.

XX

PI Koehler RH;

XX

DR WPI; 2002-463314/49.

DR N-PSDB; ABK52891.

XX

PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.

XX

PS Claim 1; Fig 2; 94pp; English.

XX

CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents the human netrin binding

CC membrane receptor UNC5H-1 protein of the invention

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 682; DB 5; Length 898;

Best Local Similarity 100.0%; Pred. No. 5e-52;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNVQKTAC 60
|||||

Db 232 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNVQKTAC 291

Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDL 117
|||||

Db 292 ATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDL 348

RESULT 5

ADH71618

ID ADH71618 standard; protein; 898 AA.

XX

AC ADH71618;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21e SEQ ID NO:514.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.

AAW78898

ID AAW78898 standard; protein; 898 AA.

XX

AC AAW78898;

XX

DT 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)

XX

DE Rat UNC-5 homologue UNC5H-1.

XX

KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;

KW diagnosis; therapy.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Peptide 580. .594

FT /note= "peptide used to raise rabbit polyclonal antisera"

XX

PN W09837085-A1.

XX

PD 27-AUG-1998.

XX

PF 19-FEB-1998; 98WO-US003143.

XX

PR 19-FEB-1997; 97US-00808982.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;

XX

DR WPI; 1998-495364/42.

DR N-PSDB; AAV52940.

XX

PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
PT the biopharmaceutical industry.

XX

PS Claim 1; Page 19-22; 32pp; English.

XX

CC UNC5H-1 and UNC5H-2 (see AAW78900) are rat homologues of Caenorhabditis
CC elegans UNC-5 protein. Their amino acid sequences were deduced from
CC isolated unc5h cDNA clones (see AAV52940 and AAV52942) isolated from an
CC El8 brain cDNA library. The predicted proteins show similarity with UNC-
CC 5, possess 2 predicted Ig-like domains and 2 predicted thrombospondin
CC type-1 repeats, a predicted membrane spanning region, and a large
CC intracellular domain. They are predicted to be involved in cell migration
CC and axon guidance, and are characterised as receptor proteins for
CC netrins. Human UNC5H-1 (see AAW78899) and UNC5H-2 (see AAW78901) proteins
CC are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly
CC from transfected host cells. The invention also provides unc-5
CC hybridisation probes and primers, vertebrate UNC-5-specific binding
CC agents such as specific antibodies, and methods of making and using the
CC subject compositions in diagnosis (e.g. genetic hybridisation screens for
CC vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate
CC vertebrate unc-5 gene expression) and in the biopharmaceutical industry
CC (e.g. as immunogens, reagents for modulating cell guidance, reagents for
CC screening chemical libraries for lead pharmacological agents, etc.).

diagnosing and/or developing treatments for schizophrenia using chronic animal models. The polynucleotides and their encoded polypeptides are used for identification of compounds which modulate the expression of YSG molecules, leading to the manufacture of schizophrenia medicaments. The sequences can also be used for testing candidate compounds for any effect on the polypeptides. Anti-schizophrenic effects of a compound can be determined by measuring local cerebral glucose utilisation (LCGU) or comparing its expression level with that of a control group. The sequences are useful in the identification of genes associated with schizophrenic states and in the development of an antibody. The sequences of the invention include phosphodiesterase 1-alpha, calcium-independent alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain receptor 1 (trkE), netrin receptor (UNC5H1), synapsins 1A and AB and tumour necrosis factor (TNF) alpha. This sequence represents rat netrin receptor UNC5H1 (YSG7) polypeptide

SQ Sequence 898 AA;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNQKTAC 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 232 STSAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNQKTAC 291

Qy 61 ATLCVPDGSWSPWSKWSACGLDCTHWSRECS DPAPRNNGEECQGTDLDRNCTSDL 117
| | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | |
Db 292 ATLCVPDGSWSSWSKWSACGLDCTHWSRECS DPAPRNNGEECRGADLDTRNCTSDL 348

AAU97900

XX

AC AAU97900;

DT 27-AUG-2002 (first entry)

DE Rat netrin binding membrane receptor UNC5H-1 protein.

KW Netrin binding membrane receptor; receptor; UNC5H-1; Rat; nootropic;
KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
KW central nervous system; CNS; stroke; Parkinson's disease;
KW multiple sclerosis; Alzheimer's disease.

OS Rattus sp.

FH	Key	Location/Qualifiers
FT	Domain	152. .223
FT		/note= "Immunoglobulin domain "
FT	Domain	247. .294
FT		/note= "Thrombospondine type 1 domain "
FT	Domain	302. .348
FT		/note= "Thrombospondine type 1 domain"
FT	Region	361. .382
FT		/note= "Transmembrane region"


```
FT      Domain      495.  .598
FT      /note= "ZU5 domain"
FT      Domain      817.  .897
FT      /note= "Death domain"
```

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.

XX

PA (FARB) BAYER AG.

XX

PI Koehler RH;

XX

DR WPI; 2002-463314/49.

XX

PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.

XX

PS Disclosure; Fig 3; 94pp; English.

XX

CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents the Rat netrin binding
CC membrane receptor UNC5H-1 protein of the invention

XX

SQ Sequence 898 AA;

Query Match 96.9%; Score 661; DB 5; Length 898;

Best Local Similarity 96.6%; Pred. No. 3.6e-50;

Matches 113; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGONVQKTAC 60

[illegible]

Db 232 STSAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRCTNPAPLNGGAFCEGQNVQKTAC 291

Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECOGTDLDTRNCTSDL 117

[illegible]

RESULT 9

ADG42580

ID ADG42580 standard; protein; 898 AA.

XX

AC ADG42580;

XX

DT 26-FEB-2004 (first entry)

XX

DE Rat transmembrane receptor Unc5H1.

XX

KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;

KW NOVX-associated disorder; cancer; rat; transmembrane receptor; Unc5H1.

XX

OS Rattus norvegicus.

XX

PN US2003204052-A1.

XX

PD 30-OCT-2003.

XX

PF 04-OCT-2001; 2001US-00970944.

XX

PR 04-OCT-2000; 2000US-0237862P.

XX

PA (HERR/) HERRMANN J L.

PA (RAST/) RASTELLI L.

PA (SHIM/) SHIMKETS R A.

XX

PI Herrmann JL, Rastelli L, Shimkets RA;

XX

DR WPI; 2003-900673/82.

XX

PT New NOVX gene or NOVX-specific antibody, useful for preparing a
PT composition for treating or preventing a NOVX-associated disorder, e.g.,
PT cancer.

XX

PS Disclosure; SEQ ID NO 13; 118pp; English.

XX

CC The invention describes a new isolated polypeptide comprising: a
CC polypeptide or its mature form comprising a sequence not given in the
CC specification; or a variant of (A), where one or more amino acid residues
CC in the variant differs in no more than 15% from the amino acid sequence
CC of the mature form. The pharmaceutical composition may be administered
CC via oral, transdermal, rectal or parenteral route. The polypeptide,
CC nucleic acid or antibody is useful for preparing a composition for
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
CC the amino acid sequence of a transmembrane receptor Unc5H1 used in a
CC comparison with the novel human proteins of the invention.

XX

SQ Sequence 898 AA;

Query Match 96.9%; Score 661; DB 7; Length 898;

Best Local Similarity 96.6%; Pred. No. 3.6e-50;

Matches 113; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

Sequence 943 AA;

RESULT 11

PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.

PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71611.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 508; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 331 AA;

Query Match 91.3%; Score 622.5; DB 8; Length 331;
Best Local Similarity 92.4%; Pred. No. 3.4e-47;
Matches 109; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

```
Qy      1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNV-QKTA 59
      |||
Db      207 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNVHDRTV 266

Qy      60 CATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDL 117
      : | |||
Db      267 SLLVSV DGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDL 324
```

RESULT 12

ADH71626

ID ADH71626 standard; protein; 898 AA.

XX

AC ADH71626;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21i SEQ ID NO:522.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX

RESULT 14

ADG42569

ID ADG42569 standard; protein; 899 AA.

XX

AC ADG42569;

XX

DT 26-FEB-2004 (first entry)

XX

DE Novel human NOV1.

XX

KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;

KW NOVX-associated disorder; cancer; human.

XX

OS Homo sapiens.

XX

PN US2003204052-A1.

XX

PD 30-OCT-2003.

XX

PF 04-OCT-2001; 2001US-00970944.

XX

PR 04-OCT-2000; 2000US-0237862P.

XX

PA (HERR/) HERRMANN J L.

PA (RAST/) RASTELLI L.

PA (SHIM/) SHIMKETS R A.

XX

PI Herrmann JL, Rastelli L, Shimkets RA;

XX

DR WPI; 2003-900673/82.

DR N-PSDB; ADG42568.

XX

PT New NOVX gene or NOVX-specific antibody, useful for preparing a
 PT composition for treating or preventing a NOVX-associated disorder, e.g.,
 PT cancer.

XX

PS Claim 1; SEQ ID NO 2; 118pp; English.

XX

CC The invention describes a new isolated polypeptide comprising: a
 CC polypeptide or its mature form comprising a sequence not given in the
 CC specification; or a variant of (A), where one or more amino acid residues
 CC in the variant differs in no more than 15% from the amino acid sequence
 CC of the mature form. The pharmaceutical composition may be administered
 CC via oral, transdermal, rectal or parenteral route. The polypeptide,
 CC nucleic acid or antibody is useful for preparing a composition for
 CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
 CC the amino acid sequence of a human NOVX protein.

XX

SQ Sequence 899 AA;

Query Match 91.3%; Score 622.5; DB 7; Length 899;

Best Local Similarity 92.4%; Pred. No. 9.5e-47;

Matches 109; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNV-QKTA 59
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 Db 232 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVHDRTV 291
 Qy 60 CATLCPVDGWSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDL 117
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RESULT 15

ADH71636

ID ADH71636 standard; protein; 899 AA.

XX

AC ADH71636;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21n SEQ ID NO:532.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
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PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
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PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
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PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:42:47 ; Search time 7.01044 Seconds
(without alignments)
1245.848 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
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1	661	96.9	898	2	US-08-808-982-5	Sequence 5, Appli	
2	661	96.9	898	3	US-09-306-902A-5	Sequence 5, Appli	
3	539	79.0	769	4	US-09-949-016-10665	Sequence 10665, A	
4	522	76.5	943	2	US-08-808-982-7	Sequence 7, Appli	
5	522	76.5	943	3	US-09-306-902A-7	Sequence 7, Appli	
6	266	39.0	1172	1	US-08-313-288B-19	Sequence 19, Appl	
7	266	39.0	1172	4	US-09-949-016-6333	Sequence 6333, Ap	
8	262	38.4	1170	4	US-09-657-472-2	Sequence 2, Appli	
9	261.5	38.3	939	4	US-09-854-845-16	Sequence 16, Appl	
10	261.5	38.3	954	4	US-09-854-845-14	Sequence 14, Appl	
11	261.5	38.3	1034	4	US-09-854-845-6	Sequence 6, Appli	

12	261.5	38.3	1049	4	US-09-854-845-2	Sequence 2, Appli
13	261.5	38.3	1078	4	US-09-854-845-8	Sequence 8, Appli
14	261.5	38.3	1093	4	US-09-854-845-4	Sequence 4, Appli
15	261.5	38.3	1136	4	US-09-854-845-12	Sequence 12, Appl
16	261.5	38.3	1151	4	US-09-854-845-10	Sequence 10, Appl
17	258	37.8	239	5	PCT-US93-01652-1	Sequence 1, Appli
18	258	37.8	1170	1	US-08-313-288B-20	Sequence 20, Appl
19	243	35.6	469	1	US-08-313-288B-15	Sequence 15, Appl
20	243	35.6	484	4	US-09-949-016-9698	Sequence 9698, Ap
21	240.5	35.3	479	4	US-09-270-767-46823	Sequence 46823, A
22	232.5	34.1	1045	4	US-09-949-016-11112	Sequence 11112, A
23	230.5	33.8	441	3	US-08-985-526-3	Sequence 3, Appli
24	226.5	33.2	218	3	US-08-985-526-1	Sequence 1, Appli
25	191	28.0	788	2	US-08-918-914-4	Sequence 4, Appli
26	182	26.7	552	4	US-09-969-532-8	Sequence 8, Appli
27	182	26.7	563	4	US-09-969-532-6	Sequence 6, Appli
28	182	26.7	566	4	US-09-969-532-4	Sequence 4, Appli
29	182	26.7	577	4	US-09-969-532-2	Sequence 2, Appli
30	182	26.7	886	4	US-09-969-532-16	Sequence 16, Appl
31	182	26.7	897	4	US-09-969-532-14	Sequence 14, Appl
32	182	26.7	900	4	US-09-969-532-12	Sequence 12, Appl
33	182	26.7	911	4	US-09-969-532-10	Sequence 10, Appl
34	177	26.0	321	4	US-09-969-532-24	Sequence 24, Appl
35	177	26.0	332	4	US-09-969-532-22	Sequence 22, Appl
36	177	26.0	335	4	US-09-969-532-20	Sequence 20, Appl
37	177	26.0	346	4	US-09-969-532-18	Sequence 18, Appl
38	177	26.0	655	4	US-09-969-532-32	Sequence 32, Appl
39	177	26.0	666	4	US-09-969-532-30	Sequence 30, Appl
40	177	26.0	669	4	US-09-969-532-28	Sequence 28, Appl
41	177	26.0	680	4	US-09-969-532-26	Sequence 26, Appl
42	166	24.3	481	4	US-09-130-491-8	Sequence 8, Appli
43	165	24.2	1224	4	US-09-930-872-4	Sequence 4, Appli
44	165	24.2	1224	4	US-10-217-774-4	Sequence 4, Appli
45	161	23.6	905	3	US-09-369-364A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-08-808-982-5

; Sequence 5, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA


```

;      ZIP: 94104
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/808,982
;      FILING DATE:
;      CLASSIFICATION: 530
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;      INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 898 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: not relevant
;      TOPOLOGY: not relevant
;      MOLECULE TYPE: peptide
US-08-808-982-5

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Query Match          96.9%; Score 661; DB 2; Length 898;
Best Local Similarity 96.6%; Pred. No. 7.5e-57;
Matches 113; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db      232 STSAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPPAPLNGGAFCEGQNVQKTAC 291

Qy      61 ATLC PVDG SWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDL 117
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      292 ATLC PVDG SWSSWSKWSACGLDCTHWSRECS DPAPRNGGEECRGADLDTRNCTSDL 348

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RESULT 2

US-09-306-902A-5

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; Sequence 5, Application US/09306902A
; Patent No. 6277585

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GENERAL INFORMATION:

```

;      APPLICANT: Tessier-Lavigne, Marc
;                  Leonardo, E. David
;                  Hink, Lindsay
;                  Masu, Masayuki
;                  Kazuko, Keino-Masu
;      TITLE OF INVENTION: Netrin Receptors
;      NUMBER OF SEQUENCES: 9
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;                  STREET: 268 BUSH STREET, SUITE 3200
;                  CITY: SAN FRANCISCO
;                  STATE: CALIFORNIA
;                  COUNTRY: USA

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10665
;   LENGTH: 769
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10665
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Db 88 STTATVIVYVNGGWSTWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIA 147

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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-7

Query Match 76.5%; Score 522; DB 2; Length 943;
Best Local Similarity 71.8%; Pred. No. 3.7e-43;
Matches 84; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTAC 60
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Db 234 STTATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQACQKTAC 293

Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDTNCTSDL 117
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Db 294 TTVCVPDGAWTEWSKWSACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGL 350

RESULT 5

US-09-306-902A-7

; Sequence 7, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342

```
; INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 943 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: not relevant
;         TOPOLOGY: not relevant
;     MOLECULE TYPE: peptide
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US-09-306-902A-7
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Best Local Similarity 71.8%; Pred. No. 3.7e-43;
Matches 84; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
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Db      234 STTATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQACQKTAC 293

Qy      61 ATLCVPDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDRNCTSDL 117
      |:|||||:|: ||||| | ||||| | ||||:| || ||||:| |
Db      294 TTVCVPDGAWTEWSKWSACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGL 350
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RESULT 6

US-08-313-288B-19

; Sequence 19, Application US/08313288B

; Patent No. 5750502

; GENERAL INFORMATION:

; APPLICANT: Jessell, Thomas M. and AviHu Klar

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A

; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,288B

; FILING DATE: January 5, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; TELEX:

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1172 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-313-288B-19

Query Match 39.0%; Score 266; DB 1; Length 1172;
Best Local Similarity 43.9%; Pred. No. 7.2e-18;
Matches 47; Conservative 14; Mismatches 42; Indels 4; Gaps 2;

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Db 437 DGGWSHWSPWSSCSVTCGVGNITRIRLCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGR 496

Qy 70 WSPWSKWSACGLDCT---HWSRECS DPAPRNGGEECQGTDL DTRNC 113

|||| | ||| : | | :| |: | |: ||: | | : : |

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RESULT 7

US-09-949-016-6333

; Sequence 6333, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6333

; LENGTH: 1172

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6333

Query Match 39.0%; Score 266; DB 4; Length 1172;
Best Local Similarity 43.9%; Pred. No. 7.2e-18;
Matches 47; Conservative 14; Mismatches 42; Indels 4; Gaps 2;

Qy 11 NGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGS 69
:|||| |: || || :|| | | | |: | | | : || ||: ||

Db 437 DGGWSHWSPWSSCSVTCGVGNITRIRLCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGR 496

Qy 70 WSPWSKWSACGLDCT---HWSRECS DPAPRNGGEECQGTDL DTRNC 113

|||| | ||| : | | :| |: | |: ||: | | : : |

RESULT 8

US-09-657-472-2

; Sequence 2, Application US/09657472
 ; Patent No. 6727063
 ; GENERAL INFORMATION:
 ; APPLICANT: Lander, Eric S.
 ; APPLICANT: Cargill, Michele
 ; APPLICANT: Ireland, James S.
 ; APPLICANT: Bolk, Stacey
 ; APPLICANT: Daley, George Q.
 ; APPLICANT: McCarthy, Jeanette J.
 ; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
 ; FILE REFERENCE: 2825.1027-001
 ; CURRENT APPLICATION NUMBER: US/09/657,472
 ; CURRENT FILING DATE: 2000-09-07
 ; PRIOR APPLICATION NUMBER: US 60/153,357
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 60/220,947
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: US 60/225,724
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 2551
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1170
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-657-472-2

Query Match 38.4%; Score 262; DB 4; Length 1170;
 Best Local Similarity 42.1%; Pred. No. 1.8e-17;
 Matches 45; Conservative 17; Mismatches 41; Indels 4; Gaps 2;

Qy 11 NGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGS 69
 :|||| |: || || :|| | | | :|:| | ||| : || ||::|
 Db 435 DGGWSHWSPWSSCSVTCGDGVITRIRLCNSPSPQMNGKPCGEARETKACKKDACPINGG 494
 Qy 70 WSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTNRC 113
 | ||| | | : | ||| |::|||: ||::| | : : |
 Db 495 WGPWSPWDICSVTCGGGVQKRSLCNPAPQFGGKDCVGDVTENQIC 541

RESULT 9

US-09-854-845-16

; Sequence 16, Application US/09854845
 ; Patent No. 6750054
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wang, Xiaoming
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
 Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0177-USA

```
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 939
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-16
```

RESULT 10

Query Match 38.3%; Score 261.5; DB 4; Length 954;
Best Local Similarity 47.6%; Pred. No. 1.6e-17;
Matches 50; Conservative 9; Mismatches 41; Indels 5; Gaps 3;


```

Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNVQKTACAT-LCPVDG 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      712 VRGAWSCWTSWSPCSASCGGGHYQRTSRCTSPAPSPGEDICLGLHTEEALCATQACP--E 769

Qy      69 SWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDT RNC 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      770 GWSPWSEWSKCTDDGAQSR SRHCEELL P--GSSACAGNSSQSRPC 812

```

RESULT 11

```

US-09-854-845-6
; Sequence 6, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-6

```

```

Query Match          38.3%; Score 261.5; DB 4; Length 1034;
Best Local Similarity 47.6%; Pred. No. 1.7e-17;
Matches 50; Conservative 9; Mismatches 41; Indels 5; Gaps 3;

```

```

Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNVQKTACAT-LCPVDG 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      807 VRGAWSCWTSWSPCSASCGGGHYQRTSRCTSPAPSPGEDICLGLHTEEALCATQACP--E 864

Qy      69 SWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDT RNC 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      865 GWSPWSEWSKCTDDGAQSR SRHCEELL P--GSSACAGNSSQSRPC 907

```

RESULT 12

```

US-09-854-845-2
; Sequence 2, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.

```

```
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-2
```

```
Query Match          38.3%; Score 261.5; DB 4; Length 1049;
Best Local Similarity 47.6%; Pred. No. 1.8e-17;
Matches 50; Conservative 9; Mismatches 41; Indels 5; Gaps 3;
```

```
Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRCTNPAPLNGGAFCEGQNVQKTACAT-LCPVDG 68
      | | | | | | | | | | | | | | : | : | : | | | | | : : | | | |
Db      807 VRGAWSCWTSWSPCSASC GG GHYQRTSRCTSPAPSPGEDICLGLHTEEALCATQACP--E 864

Qy      69 SWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDT RNC 113
      | | | | : | | | | | | | | : | |
Db      865 GWSPWSEWSKCTDDGAQSR SRHCEELP--GSSACAGNSSQSRPC 907
```

RESULT 13

```
US-09-854-845-8
; Sequence 8, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-8
```

```
Query Match          38.3%; Score 261.5; DB 4; Length 1078;
```

Best Local Similarity 47.6%; Pred. No. 1.8e-17;
Matches 50; Conservative 9; Mismatches 41; Indels 5; Gaps 3;

```
Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPPAPLNGGAFCEGQNVQKTACAT-LCPVDG 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      851 VRGAWSCWTSWSPCSASC GG GGHYQRTSRCTSPAPSPGEDICLGLHTEEALCATQACP--E 908

Qy      69 SWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDL DTRNC 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      909 GWSPWSEWSKCTDDGAQSRSRHCEELLP--GSSACAGNSSQSRPC 951
```

RESULT 14

US-09-854-845-4

; Sequence 4, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1093
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-4

Query Match 38.3%; Score 261.5; DB 4; Length 1093;
Best Local Similarity 47.6%; Pred. No. 1.8e-17;
Matches 50; Conservative 9; Mismatches 41; Indels 5; Gaps 3;

```
Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPPAPLNGGAFCEGQNVQKTACAT-LCPVDG 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      851 VRGAWSCWTSWSPCSASC GG GGHYQRTSRCTSPAPSPGEDICLGLHTEEALCATQACP--E 908

Qy      69 SWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDL DTRNC 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      909 GWSPWSEWSKCTDDGAQSRSRHCEELLP--GSSACAGNSSQSRPC 951
```

RESULT 15

US-09-854-845-12

; Sequence 12, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade

```
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1136
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-12
```

```
Query Match          38.3%; Score 261.5; DB 4; Length 1136;
Best Local Similarity 47.6%; Pred. No. 1.9e-17;
Matches    50; Conservative    9; Mismatches    41; Indels    5; Gaps    3;
```

```
Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPPAPLNGGAFCEGQNVQKTACAT-LCPVDG 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      909 VRGAWSCWTSWSPCSASCGGGHYQRTSRCTSPAPSPGEDICLGLHTEEALCATQACP--E 966

Qy      69 SWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDT RNC 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      967 GWSPWSEWSKCTDDGAQSRSRHCEELP--GSSACAGNSSQSRPC 1009
```

```
Search completed: March 1, 2005, 09:05:51
Job time : 8.01044 secs
```

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:46:18 ; Search time 4.56741 Seconds
 (without alignments)
 2464.715 Million cell updates/sec

Title: US-10-624-932-2_COPY_232_348
 Perfect score: 682
 Sequence: 1 SASAAVIVYVNGGWSTWTEW.....NGGEECQGTDLDTNCTSDL 117

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	303	44.4	919	2	T32541	unc-5 protein - Ca
2	303	44.4	947	1	B44294	unc-5 protein, lon
3	284	41.6	1074	2	JC5928	semaphorin F precu
4	271	39.7	1172	2	A42587	thrombospondin 2 p
5	269.5	39.5	1584	2	T00026	brain-specific ang
6	268	39.3	984	2	T00326	hypothetical prote
7	268	39.3	1522	2	T00028	brain-specific ang
8	266	39.0	1172	1	TSHUP2	thrombospondin 2 p
9	258	37.8	1170	1	TSHUP1	thrombospondin 1 p
10	258	37.8	1170	2	A40558	thrombospondin 1 p
11	254.5	37.3	1444	2	T18856	angiogenesis inhib
12	251.5	36.9	1178	1	A39804	thrombospondin pre
13	243	35.6	469	1	S29126	properdin precurs

14	242	35.5	1572	2	T00027	brain-specific ang
15	229	33.6	437	2	S05478	properdin - mouse
16	220	32.3	254	2	T15952	hypothetical prote
17	191	28.0	788	2	T25061	hypothetical prote
18	178.5	26.2	957	2	T15976	hypothetical prote
19	165.5	24.3	152	2	D89753	protein FllC7.2 [i
20	159	23.3	805	2	T34212	hypothetical prote
21	157.5	23.1	837	2	T00355	hypothetical prote
22	156	22.9	584	1	C8HUA	complement C8 alph
23	154.5	22.7	951	2	T00017	gene ADAMTS-1 prot
24	154	22.6	2165	2	T21371	hypothetical prote
25	152	22.3	654	2	T29247	hypothetical prote
26	151.5	22.2	860	2	T16892	hypothetical prote
27	151	22.1	934	1	A34372	complement C6 prec
28	148.5	21.8	590	2	I46687	complement compone
29	148	21.7	591	1	C8HUB	complement C8 beta
30	147.5	21.6	550	2	T47158	hypothetical prote
31	143.5	21.0	585	2	I46686	complement compone
32	143.5	21.0	807	2	A38152	F-spondin - rat
33	143.5	21.0	1205	2	T18517	procollagen N-endo
34	142.5	20.9	206	2	A45517	coccidiosis-relate
35	142.5	20.9	712	2	A45638	immunodominant mic
36	140.5	20.6	843	1	A27340	complement C7 prec
37	138	20.2	724	2	A48569	antigen Em100 - Ei
38	132.5	19.4	803	2	A47723	F-spondin precurs
39	130	19.1	334	2	T20524	hypothetical prote
40	128.5	18.8	1360	2	T33922	hypothetical prote
41	114	16.7	293	2	T20523	hypothetical prote
42	109.5	16.1	651	2	T19477	hypothetical prote
43	109.5	16.1	736	2	T19366	hypothetical prote
44	108	15.8	951	2	T00260	hypothetical prote
45	106.5	15.6	610	2	T16761	hypothetical prote

ALIGNMENTS

RESULT 1

T32541

unc-5 protein - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T32541

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32541

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-919 <LAT>

A;Cross-references: UNIPROT:O44171; EMBL:AF036698; PIDN:AAB88355.1;

GSPDB:GN00022; CESP:B0273.4a

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5; CESP:B0273.4a

A;Map position: 4

A;Introns: 41/3; 108/1; 142/3; 201/1; 323/2; 553/1; 858/3
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology;
thrombospondin type 1 repeat homology

Query Match 44.4%; Score 303; DB 2; Length 919;
Best Local Similarity 40.6%; Pred. No. 9.4e-19;
Matches 52; Conservative 17; Mismatches 43; Indels 16; Gaps 2;

```
Qy      6 VIVYVNGGWSTWTEW-SVCSASCG-----RGWQKRSRSTNPAPLNGGAF 49
      | :||:|||| |: | | | | | | | | | | | | | | | | | | | | | |
Db      197 VQIYVDGGWSEWSPWIGTCHVDCPLL RQHAHRIRDPHDVLP HQRRTRTCNNPAPLNDGEY 256

Qy      50 CEGQNQKTACATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL D 109
      |:|: :| | :|| || || || | | | | | | | | | | | | | | | | |
Db      257 CKGEEEMTRSCKVPCKLDGGWSSWSDWSACSSSCHRYRTRACTVPPPMNGGQPCFGDDLM 316

Qy      110 TRNCTSDL 117
      |: | : |
Db      317 TQECPAQL 324
```

RESULT 2

B44294

unc-5 protein, long form - *Caenorhabditis elegans*

N;Contains: unc-5 protein, short form

C;Species: *Caenorhabditis elegans*

C;Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004

C;Accession: B44294; T32540; A44294

R;Leung-Hagesteijn, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.;

Hedgecock, E.M.; Culotti, J.G.

Cell 71, 289-299, 1992

A;Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin type 1 domains, guides cell and pioneer axon migrations in *C. elegans*.

A;Reference number: A44294; MUID:93046629; PMID:1384987

A;Contents: variety Bergerac

A;Accession: B44294

A;Molecule type: DNA

A;Residues: 1-947 <LEU>

A;Cross-references: UNIPROT:O44171; GB:S47168; NID:g258527; PIDN:AAB23867.1; PID:g258529

A;Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670, NCBIN:116672, NCBIN:116674, NCBIN:116676, NCBIN:116678, NCBIN:116680, NCBIN:116682, NCBIN:116685, NCBIP:118648)

A;Note: authors translated the codon CTA for residue 642 as Val; sequence shown follows the authors' translation

A;Note: mRNA lacking the first exon is equally prevalent

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32540

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-947 <LAT>

A;Cross-references: EMBL:AF036698; PIDN:AAB88356.1; GSPDB:GN00022; CESP:B0273.4b

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5
 A;Map position: 4
 A;Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3
 C;Function:
 A;Description: required for guidance of pioneering axons and cells migrating dorsally along the body wall; proposed to be a receptor on the surface of the motile cells
 C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin type 1 repeat homology
 C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
 F;30-947/Product: unc-5 protein, short form #status predicted <ALT>
 F;46-116/Domain: immunoglobulin homology <IM1>
 F;153-211/Domain: immunoglobulin homology <IM2>
 F;229-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>
 F;301-354/Domain: thrombospondin type 1 repeat homology <THR2>
 F;365-390/Domain: transmembrane #status predicted <TMM>
 F;512-559/Domain: SH3 homology <SH3>
 F;53-114,65-112,160-209/Disulfide bonds: #status predicted
 F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.4%; Score 303; DB 1; Length 947;
 Best Local Similarity 40.6%; Pred. No. 9.7e-19;
 Matches 52; Conservative 17; Mismatches 43; Indels 16; Gaps 2;

```

Qy      6 VIVYVNGGWSTWTEW-SVCSASCG-----RGWQKRSRSCNTPAPLNGGAF 49
      | :||:|||| |: | | | | | | | | | | | | | | | | | | | | | |
Db      225 VQIYVDGGWSEWSPWIGTCHVDCPLL RQHAHRIRDPHDVLP HQRRTRTCNNPAPLNDGEY 284

Qy      50 CEGQNVQKTACATLCPVDGWSWPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDL D 109
      |:|: :| | :|| || || || | | | | | | | | | | | | | | | | |
Db      285 CKGEEEMTRSCCKVPCKLDGGWSSWSDWSACSSSCHRYRTRACTVPPPMNGGQPCFGDDL M 344

Qy      110 TRNCTSDL 117
      |: | : |
Db      345 TQECPAQL 352
  
```

RESULT 3

JC5928

semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: JC5928

R;Simmons, A.D.; Puschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.

Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: UNIPROT:Q13591; GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584

A;Experimental source: brain

C;Comment: This protein disrupts normal brain development and leads to some of the features of Cri-du-chat.

C;Genetics:

A;Gene: sema4

C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>

F;50-533/Domain: semaphorin #status predicted <SEM>

F;840-896/Domain: thrombospondin type 1 repeat homology <THR3>

F;971-993/Domain: transmembrane #status predicted <TMM>

Query Match 41.6%; Score 284; DB 2; Length 1074;

Best Local Similarity 46.4%; Pred. No. 4.6e-17;

Matches 51; Conservative 11; Mismatches 44; Indels 4; Gaps 2;

```
Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACATL-CPVDG 68
      ||| || || || || | || : | | | || | || | | :: | || |||||
Db      783 VNGAWSAWTSWSQCSRDCSRGIRNRKRVCNNPEPKYGGMPCLGPSLEYQECNTLPCPVDG 842

Qy      69 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTNRNCTS 115
      || || |: | | : |:| ||:|||| ||: | | : | :
Db      843 VWSCWSPWTKSATCGGGHYMRTRSCSNPAPAYGGDICLGLHTEELCNT 892
```

RESULT 4

A42587

thrombospondin 2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A42587; A39851

R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992

A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development.

A;Reference number: A42587; MUID:92147683; PMID:1371115

A;Accession: A42587

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-1172 <LAH>

A;Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:g340421;
PIDN:AAA53064.1; PID:g567241

A;Note: sequence extracted from NCBI backbone (NCBIP:81502)

R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.;
Dixit, V.M.

J. Biol. Chem. 266, 12821-12824, 1991

A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.

A;Reference number: A39851; MUID:91302287; PMID:1712771

A;Accession: A39851

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-873 <BOR>

A;Cross-references: GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:g201995

C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding; glycoprotein

F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>

F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>

F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF1>
F;652-691/Domain: EGF homology <EGF>

Query Match 39.7%; Score 271; DB 2; Length 1172;
Best Local Similarity 44.9%; Pred. No. 6.6e-16;
Matches 48; Conservative 13; Mismatches 42; Indels 4; Gaps 2;

Qy	11	NGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCGQNVQKTAC-ATLCPVDGS	69
		: : : : : :	
Db	437	NGGWSHWSPWSSCSVTCGVGNVTRI RL CNSPVPQMGGKNCKGSGRETKPCQRDPCPIDGR	496
Qy	70	WSPWSKWSACGLDCT---HWSRECS DPAPRNGGEECQGTDL DTRNC	113
		: : : :: : :	
Db	497	WSPWSPWSACTVTCAGGIRERSRVCNSPEPOYGGKDCVGDVTEHOMC	543

RESULT 5

T00026

brain-specific angiogenesis inhibitor 1 - human

N;Alternate names: BAI1 protein

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1999 #sequence revision 22-Jan-1999 #text change 09-Jul-2004

C;Accession: T00026

R;Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kimura, Y.; Kiyono, K.; Tatsumi, K.; Yoshida, S.; Ono, M.; Kuwano, M.; Nakamura, Y.

submitted to the EMBL Data Library, June 1997

A;Reference number: Z14064

A;Accession: T00026

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1584 <NIS>

A;Cross-references: UNIPROT:O14514; EMBL:AB005297; NID:d1175078; PID:d1024528

A; Experimental source: brain

C; Genetics:

A;Gene: GDB:BAI1

A;Cross-references: GDB:9838088; OMIM:602682

A;Map position: 8q24-8q24

F;408-462/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 39.5%; Score 269.5; DB 2; Length 1584;
Best Local Similarity 45.9%; Pred. No. 1.1e-15;
Matches 51; Conservative 18; Mismatches 31; Indels 11; Gaps 5;

```

Qy      10 VNGGWSTWTEWSVCASACGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTAC-ATLCP--- 65
      |:| | |: ||:|::|||:: |:|:| | || ||| | | |||
Db      408 VHGAWDEWSPWSLCSSTCGRGFRDTRTCR--PPQFGGNPCEGPEKQTKFCNIALCPGRA 465

Qy      66 VDGSWSPWSKWSACGLDCT---HWSRECSDPAPRNGGEECQGTDLDRNC 113
      |||:|: || |||| |: |:|:|: |: || |||| ::|:|
Db      466 VDGNNWNEWSSWSACSASCSOGROORTRECNGPS--YGGAECOGHWVETRDC 514

```

RESULT 6

T00326

hypothetical protein KIAA0550 - human

Query Match 39.3%; Score 268; DB 2; Length 1522;
Best Local Similarity 46.3%; Pred. No. 1.5e-15;
Matches 50; Conservative 13; Mismatches 37; Indels 8; Gaps 4;

```
Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTAC-ATLCPVDG 68
      |:| | |: ||:| | :||| | |:||| | | || ||| | | |||||
Db      344 VHGVWEEWSPWSLCSFTCGRGQRTTRTSCT--PPQYGGRPCEGPETHHKPCNIALCPVDG 401

Qy      69 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTTRNC 113
      | || || | : | | |||:| : | | |||:| :| | |
Db      402 QWQEWSWSQCSVTCSNGTQQRSRQCT--AAAHHGGSECRGPWAESREC 447
```

RESULT 8

TSHUP2

thrombospondin 2 precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: A47379; A42173

R;LaBell, T.L.; Byers, P.H.

Genomics 17, 225-229, 1993

A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: potential regulatory role for the 3' untranslated region.

A;Reference number: A47379; MUID:94010892; PMID:8406456

A;Accession: A47379

A;Molecule type: mRNA

A;Residues: 1-1172 <LAB>

A;Cross-references: UNIPROT:P35442; GB:L12350; NID:g307505; PIDN:AAA03703.1; PID:g307506

R;LaBell, T.L.; Milewicz, D.J.; Disteché, C.M.; Byers, P.H.

Genomics 12, 421-429, 1992

A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression of a second member of the thrombospondin gene family in humans.

A;Reference number: A42173; MUID:92217961; PMID:1559694

A;Accession: A42173

A;Molecule type: mRNA

A;Residues: 560-1172 <LA2>

A;Cross-references: GB:M81339

A;Experimental source: fibroblast

A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)

C;Genetics:

A;Gene: GDB:THBS2; TSP2

A;Cross-references: GDB:128789; OMIM:188061

A;Map position: 6q27-6q27

C;Complex: homotrimer, disulfide linked

C;Function:

A;Description: participates in cell migration and adhesion, and in platelet aggregation

C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology

C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-1172/Product: thrombospondin 2 #status predicted <MAT>

F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>

F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>

F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
 F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
 F;553-588/Domain: EGF homology <EGF1>
 F;652-691/Domain: EGF homology <EGF>
 F;928-930/Region: cell attachment (R-G-D) motif
 F;151,316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent)
 #status predicted
 F;167-226/Disulfide bonds: #status predicted
 F;266,270/Disulfide bonds: interchain #status predicted
 F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 39.0%; Score 266; DB 1; Length 1172;
 Best Local Similarity 43.9%; Pred. No. 1.8e-15;
 Matches 47; Conservative 14; Mismatches 42; Indels 4; Gaps 2;

Qy 11 NGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGS 69
 :||| | : || || :|| | | | :| | || |:| : || ||:|
 Db 437 DGGWSHWSPWSSCSVTGCGVNITRIRLCNSPVPQMGGKNCKGSGRETKACQGAPCPIDGR 496
 Qy 70 WSPWSKWSACGLDCT---HWSRECSDPAPRNGGEECQGTDLDRNC 113
 |||| | ||| : | | :| | : ||: | | : : |
 Db 497 WSPWSPWSACTVTCAGGIRERTRVCNSPEPQYGGKACVGDVQERQMC 543

RESULT 9

TSHUPl

thrombospondin 1 precursor - human

C;Species: Homo sapiens (man)

C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: A26155; A34274; A30140; A25812; A05172; A42927

R;Lawler, J.; Hynes, R.O.

J. Cell Biol. 103, 1635-1648, 1986

A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different proteins.

A;Reference number: A26155; MUID:87057617; PMID:2430973

A;Accession: A26155

A;Molecule type: mRNA

A;Residues: 1-1170 <LAW>

A;Cross-references: UNIPROT:P07996; GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138

A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing

R;Laherty, C.D.; Gierman, T.M.; Dixit, V.M.

J. Biol. Chem. 264, 11222-11227, 1989

A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.

A;Reference number: A34274; MUID:89291870; PMID:2544587

A;Accession: A34274

A;Molecule type: DNA

A;Residues: 1-166 <LAH>

A;Cross-references: GB:J04835

R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, P.; Frazier, W.A.

J. Cell Biol. 108, 729-736, 1989

A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.

A;Reference number: A30140; MUID:89139590; PMID:2918029

A;Accession: A30140
 A;Molecule type: mRNA
 A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
 A;Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465
 A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing
 R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
 Biochemistry 25, 8418-8425, 1986
 A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite proteins.
 A;Reference number: A25812; MUID:87157592; PMID:3030396
 A;Accession: A25812
 A;Molecule type: mRNA
 A;Residues: 1-83,'A',85-397 <KOB>
 A;Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:g538354
 R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
 A;Reference number: A05172; MUID:86287276; PMID:3461443
 A;Accession: A05172
 A;Molecule type: mRNA
 A;Residues: 1-83,'A',85-374,'RC' <DIX>
 A;Cross-references: GB:M14326; NID:g340005; PIDN:AAA61237.1; PID:g553801
 A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing
 R;Sun, X.; Skorstengaard, K.; Mosher, D.F.
 J. Cell Biol. 118, 693-701, 1992
 A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
 A;Reference number: A42927; MUID:92348511; PMID:1379247
 A;Accession: A42927
 A;Molecule type: protein
 A;Residues: 987-1003 <SUN>
 A;Note: Cys-992 is shown to have a free sulfhydryl
 C;Genetics:
 A;Gene: GDB:THBS1; TSP1; TSP
 A;Cross-references: GDB:120438; OMIM:188060
 A;Map position: 15q15-15q15
 A;Introns: 23/1
 A;Note: the list of introns may be incomplete
 C;Complex: homotrimer, disulfide linked
 C;Function:
 A;Description: participates in cell migration and adhesion, and in platelet aggregation
 C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology
 C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
 F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
 F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
 F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
 F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
 F;551-586/Domain: EGF homology <EGF1>
 F;650-689/Domain: EGF homology <EGF2>
 F;926-928/Region: cell attachment (R-G-D) motif
 F;171-232/Disulfide bonds: #status predicted

F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted
F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 37.8%; Score 258; DB 1; Length 1170;
Best Local Similarity 41.1%; Pred. No. 8.6e-15;
Matches 44; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

Qy 11 NGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTAC-ATLCPVDGS 69
:|||| |: || || :|| | | | :|:| | ||: : || ||::|
Db 435 DGGWSHWSPWSSCSVTCGDGVITRIRLCNSPSPQMNGKPCEGEARETKACKKDACPINGG 494

Qy 70 WSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTNRC 113
| ||| | | : | || |::| | : ||::| | : : |
Db 495 WGPWSPWDICSVTCGGGVQKRSRLCNNPTPQFGGKDCVGDVTENQIC 541

RESULT 10

A40558

thrombospondin 1 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

C;Accession: A40558; A37905; B42587; S68787

R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.

Genomics 11, 587-600, 1991

A;Title: Characterization of the murine thrombospondin gene.

A;Reference number: A40558; MUID:92128941; PMID:1774063

A;Accession: A40558

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1170 <LAW>

A;Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452;
GB:M62453; GB:M62454; GB:M62455; GB:M62456; GB:M62457; GB:M62458; GB:M62459;
GB:M62460; GB:M62461; GB:M62462; GB:M62463; GB:M62464; GB:M62465; GB:M62466;
GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:g511867; PIDN:AAA50611.1;
PID:g511869

R;Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.

J. Biol. Chem. 265, 16691-16698, 1990

A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.

A;Reference number: A37905; MUID:90375546; PMID:2398070

A;Accession: A37905

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-490 <BOR>

A;Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1;
PID:g554390

R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992

A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development.

A;Reference number: A42587; MUID:92147683; PMID:1371115

A;Accession: B42587

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1152,'P',1154-1170 <LAH>
 A;Cross-references: GB:M87276
 A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
 R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
 FEBS Lett. 387, 36-41, 1996
 A;Title: Expression and initial characterization of recombinant mouse
 thrombospondin 1 and thrombospondin 3.
 A;Reference number: S68787; MUID:96234006; PMID:8654563
 A;Accession: S68787
 A;Molecule type: protein
 A;Residues: 19-26,'X',28-37 <CHE>
 C;Complex: homotrimer, disulfide linked
 C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat
 homology; von Willebrand factor type C repeat homology
 C;Keywords: calcium binding; glycoprotein; homotrimer
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
 F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
 F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
 F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
 F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
 F;551-586/Domain: EGF homology <EGF>
 F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.8%; Score 258; DB 2; Length 1170;
 Best Local Similarity 41.1%; Pred. No. 8.6e-15;
 Matches 44; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

Qy 11 NGGWSTWTEWSVCSASCGRGWQKRSRSCNPAPLNGGAFCEGQNVQKTAC-ATLCPVDGS 69
 :||| |: || || :|| | | | :|:| | ||: : || ||:|
 Db 435 DGGWSHSPWSSCSVTCDGVTIRLCNSPSPQMNGKPCGEARETKACKKDACPINGG 494
 Qy 70 WSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTNRC 113
 | ||| | | : | ||| |:| | : ||:| | : : |
 Db 495 WGPWSPWDICSVTCGGGVQRRSRLCNPPTPQFGGKDCVGDVTENQVC 541

RESULT 11

T18856

angiogenesis inhibitor homolog - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18856; T24653

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19031

A;Accession: T18856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WIL>

A;Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028;
 CESP:C02B4.1

A;Experimental source: clone C02B4

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19917

A;Accession: T24653

A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1444 <WI2>
 A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
 A;Experimental source: clone T07C5
 C;Genetics:
 A;Gene: CESP:C02B4.1
 A;Map position: X
 A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3;
 509/3; 566/2; 625/1; 696/2; 786/3; 812/2; 878/3; 971/1; 1007/3; 1067/1; 1099/3;
 1180/3; 1273/2; 1305/1; 1363/1; 1388/2

Query Match 37.3%; Score 254.5; DB 2; Length 1444;
 Best Local Similarity 41.4%; Pred. No. 2e-14;
 Matches 46; Conservative 16; Mismatches 40; Indels 9; Gaps 4;

Qy 12 GGWSTWTEWSVCSASCG-RGWQKRSRSTNPAPLNGGAFCEGQNVQKTACA--TLC---P 65
 |||| |:||| || || | |:| |:| ||:| |:| : | :|
 Db 1187 GGWSLWSEWSSCSKDCGDTGHQIRNRMCEPIPSNRGAYCSGYSFDQRPCVMDNVCSDEK 1246
 Qy 66 VDGSWSPWSKWSACGLDCTHW---RSRECSDPAPRNGGEECQGTDLDTTRNC 113
 ||| |:|: || | | : |:| |:| | || :| |:| : |
 Db 1247 VDGGWTDWTAWSECTDYCRNGHRSRTRFCANPKPSQGGAQCTGSDFELNPC 1297

RESULT 12

A39804
 thrombospondin precursor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A39804
 R;Lawler, J.; Duquette, M.; Ferro, P.
 J. Biol. Chem. 266, 8039-8043, 1991
 A;Title: Cloning and sequencing of chicken thrombospondin.
 A;Reference number: A39804; MUID:91217026; PMID:2022631
 A;Accession: A39804
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1178 <LAW>
 A;Cross-references: UNIPROT:P35440; GB:M60853; NID:g212763; PIDN:AAA51437.1;
 PID:g212764
 C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat
 homology; von Willebrand factor type C repeat homology
 F;325-383/Domain: von Willebrand factor type C repeat homology <VWC>
 F;386-437/Domain: thrombospondin type 1 repeat homology <THR1>
 F;442-498/Domain: thrombospondin type 1 repeat homology <THR2>
 F;499-555/Domain: thrombospondin type 1 repeat homology <THR3>
 F;658-697/Domain: EGF homology <EGF>

Query Match 36.9%; Score 251.5; DB 1; Length 1178;
 Best Local Similarity 42.4%; Pred. No. 3.2e-14;
 Matches 50; Conservative 11; Mismatches 42; Indels 15; Gaps 4;

Qy 11 NGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATL-CPVDGS 69
 :|||| |:| || || :|| | | | |:| | || | | : | |||:
 Db 443 DGGWSHWSPWSSCSVTCGVGNITRIRLCNSPIPMGGKNCVGNGRETEKCEKAPCPVNGQ 502

Qy 70 WSPWSKWSACGLDC---THWRSRECS DPAPRNGGEECQGTDLDT-----RNCTSD 116
 | ||| |||| : | ||| | : | | : || : | | || | : | |
 Db 503 WGPWSPWSACTVTCGGGIRERSRLCNSPEPQYGGKPCVG---DTKQHDMCNKRDCPID 557

RESULT 13

S29126

properdin precursor [validated] - human

N;Alternate names: factor P

C;Species: Homo sapiens (man)

C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004

C;Accession: S29126; S16150; A05319; T45112; T45113

R;Nolan, K.F.; Kaluz, S.; Higgins, J.M.G.; Goundis, D.; Reid, K.B.M.

Biochem. J. 287, 291-297, 1992

A;Title: Characterization of the human properdin gene.

A;Reference number: S29126; MUID:93038568; PMID:1417780

A;Accession: S29126

A;Molecule type: DNA

A;Residues: 1-469 <NOL1>

A;Cross-references: UNIPROT:P27918; EMBL:X70872; NID:g35679; PIDN:CAA50220.1; PID:g35680

R;Nolan, K.F.; Schwaeble, W.; Kaluz, S.; Dierich, M.P.; Reid, K.B.M.

Eur. J. Immunol. 21, 771-776, 1991

A;Title: Molecular cloning of the cDNA coding for properdin, a positive regulator of the alternative pathway of human complement.

A;Reference number: S16150; MUID:91184288; PMID:2009915

A;Accession: S16150

A;Molecule type: mRNA

A;Residues: 1-456,'R',458-469 <NOL2>

A;Cross-references: EMBL:X57748

R;Reid, K.B.M.; Gagnon, J.

Mol. Immunol. 18, 949-959, 1981

A;Reference number: A05319; MUID:82195224; PMID:7341961

A;Accession: A05319

A;Molecule type: protein

A;Residues: 28-53,'Q',55-59,'G',61,'I',63;137-138,'P',140-141,'P',143-144,'X',146-148,'Y',150,'S',152,'Y',154-156,'XSXGXA';162-163,'E',165-172,'X',174-176,'X',178,'V',180;223-228,'X',230-232,'GX',235-238,'GH',241-245;248-251,'X',253-257,'P',259,'G',261,'XPP',265-266,'X',268-269;280-285,'X',287-290,'X',292,'H',294-300,'SXXX',305-307,'X',309-315,'K',317;333-341,343-357,'X',359-362,'EXE';393-404,'QK',407;421-427,'R',429-443,'TKV',447-448,'XX',451,'RX',454-455 <REI>

R;Westberg, J.; Nordin-Fredrikson, G.; Truedsson, L.; Sjöholm, A.G.; Uhlen, M. submitted to the EMBL Data Library, May 1997

A;Reference number: Z22914

A;Accession: T45112

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-54,'X',56-73,'X',75-99,'W',101-469 <WES1>

A;Cross-references: EMBL:AF005665; PIDN:AAB63280.1

A;Experimental source: genomic DNA from individual with properdin deficiency type II

A;Accession: T45113

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-60,'X',62-413,'D',415-452,'XX',455-469 <WE2>

A;Cross-references: EMBL:AF005666; PIDN:AAC51626.1

A;Experimental source: genomic DNA from individual with properdin deficiency type III
R;Hartmann, S.; Hofsteenge, J.
J. Biol. Chem. 275, 28569-28574, 2000
A;Title: Properdin, the positive regulator of complement, is highly C-mannosylated.
A;Reference number: A59360; MUID:20435812; PMID:10878002
A;Contents: annotation
A;Note: identification and location of C-mannosylation sites by mass-spectroscopy
C;Genetics:
A;Gene: GDB:PFC
A;Cross-references: GDB:120275; OMIM:312060
A;Map position: Xp11.3-Xp11.23
A;Introns: 26/1; 76/2; 135/1; 192/1; 256/1; 314/1; 378/1; 415/2
C;Complex: a mixture of homodimers, homotrimers and homotetramers
C;Function:
A;Description: protects C3 convertase (C3bBb) from rapid inactivation
A;Pathway: complement alternate pathway
C;Superfamily: human properdin precursor; thrombospondin type 1 repeat homology
C;Keywords: complement alternate pathway; glycoprotein; homodimer; homotetramer; homotrimer; plasma
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-469/Product: properdin #status experimental <MAT>
F;76-128/Domain: thrombospondin type 1 repeat homology <THR1>
F;135-191/Domain: thrombospondin type 1 repeat homology <THR2>
F;192-255/Domain: thrombospondin type 1 repeat homology <THR3>
F;256-313/Domain: thrombospondin type 1 repeat homology <THR4>
F;314-377/Domain: thrombospondin type 1 repeat homology <THR5>
F;378-440/Domain: thrombospondin type 1 repeat homology <THR6>
F;83,86,139,142,145,196,199,260,263,321,324,382,385,388/Modified site: 2'-mannosyl-tryptophan (Trp) #status experimental
F;428/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Best Local Similarity 39.5%; Pred. No. 8.1e-14;
Matches 45; Conservative 14; Mismatches 43; Indels 12; Gaps 4;

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Qy      12 GGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT--LCPVDGS 69
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Db      137 GGWSGWGPWEPCSVTCSKGTRTRRRACNHPAPKCGG-HCPGQAQSEACDTQQVCPTHGA 195

Qy      70 WSPWSKWSACGLDC-----THWRSRECSDPAP--RNGGEECQGTDLDTNRNCT 114
      | : | | : | | | | | | | | | | : | : | | : | | |
Db      196 WATWGPWTPCSASCHGGPHEPKETR SRKCSAPEPSQKPPGKPCPGLAYEQRRCT 249

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RESULT 14

T00027

brain-specific angiogenesis inhibitor 2 - human

N;Alternate names: BAI2 protein

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004

C;Accession: T00027

R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.

Cytogenet. Cell Genet. 79, 103-108, 1997

A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor 1 (BAI 1).
 A;Reference number: Z14066; MUID:98194217; PMID:9533023
 A;Accession: T00027
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1572 <SHI>
 A;Cross-references: UNIPROT:O60241; EMBL:AB005298; NID:g3021698;
 PIDN:BAA25362.1; PID:g3021699
 A;Experimental source: brain
 C;Genetics:
 A;Gene: GDB:BAI2
 A;Cross-references: GDB:9838089; OMIM:602683
 A;Map position: 1p35-1p35

Query Match 35.5%; Score 242; DB 2; Length 1572;
 Best Local Similarity 41.8%; Pred. No. 2.6e-13;
 Matches 46; Conservative 11; Mismatches 45; Indels 8; Gaps 4;

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Qy      10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACA-TLCPVDG 68
          |:| | | ||:| | || | : | |:| | :| | | :| | : | | | |
Db      351 VHGVEEWGSWSLCSRSCGRGRSRMRTCV--PPQHGGKACEGPELQTKLCSMAACPVEG 408

Qy      69 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDTNCTS 115
          | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      409 QWLEWGPWGPCSTSCANGTQQRSRKCSVAGP--AWATCTGALTDTRECSN 456
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RESULT 15

S05478

properdin - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: S05478

R;Goundis, D.; Reid, K.B.M.

Nature 335, 82-85, 1988

A;Title: Properdin, the terminal complement components, thrombospondin and the circumsporozoite protein of malaria parasites contain similar sequence motifs.

A;Reference number: S05478; MUID:88318954; PMID:3045564

A;Accession: S05478

A;Molecule type: mRNA

A;Residues: 1-437 <GOU>

A;Cross-references: UNIPROT:P11680; EMBL:X12905; NID:g53786; PIDN:CAA31389.1;
 PID:g53787

C;Complex: a mixture of homodimers, homotrimers and homotetramers

C;Function:

A;Description: protects C3 convertase (C3bBb) from rapid inactivation

A;Pathway: complement alternate pathway

C;Superfamily: human properdin precursor; thrombospondin type 1 repeat homology

C;Keywords: complement alternate pathway; glycoprotein; homodimer; homotetramer;
 homotrimer; plasma

F;45-97/Domain: thrombospondin type 1 repeat homology <THR1>

F;104-160/Domain: thrombospondin type 1 repeat homology <THR2>

F;161-224/Domain: thrombospondin type 1 repeat homology <THR3>

F;225-282/Domain: thrombospondin type 1 repeat homology <THR4>

F;283-345/Domain: thrombospondin type 1 repeat homology <THR5>

F;346-408/Domain: thrombospondin type 1 repeat homology <THR6>

F;52,55,108,111,114,165,168,229,232,290,293,350,353,356/Modified site: 2'-
mannosyl-tryptophan (Trp) #status predicted
F;366,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.6%; Score 229; DB 2; Length 437;
Best Local Similarity 40.4%; Pred. No. 1.2e-12;
Matches 46; Conservative 10; Mismatches 46; Indels 12; Gaps 4;

Qy 12 GGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTACAT--LCPVDGS 69
|||| | | || :| :| | | | |||| || | |: | || | || | :
Db 106 GGWSEWGPWGPCSVTCSKGTQIRQRVCDNPAPKCGG-HCPGEAQQSQACDTQKTCPTHGA 164

Qy 70 WSPWSKWSACGLDC-----THWRSRECSDPAPRN--GGEECQGTDLDTNCT 114
|: | || | |||| |||| : |: | | : : |:
Db 165 WASWGPWSPRSGSCLGGAQEPKETRSRSCSAPAPSHQPPGKPCSGPAYEHKACS 218

Search completed: March 1, 2005, 09:07:19
Job time : 4.56741 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 09:06:01 ; Search time 22.5184 Seconds
(without alignments)
1704.439 Million cell updates/sec

Title: US-10-624-932-2_COPY_232_348
Perfect score: 682
Sequence: 1 SASAAVIVYVNGGWSTWTEW.....NGGEECQGTDLDRNCTSDL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	682	100.0	898	10	US-09-918-779-2	Sequence 2, Appli
2	682	100.0	898	15	US-10-624-932-2	Sequence 2, Appli
3	661	96.9	898	10	US-09-933-261-5	Sequence 5, Appli
4	661	96.9	898	10	US-09-970-944-13	Sequence 13, Appl
5	661	96.9	898	14	US-10-256-702-5	Sequence 5, Appli
6	661	96.9	898	14	US-10-240-154-16	Sequence 16, Appl
7	622.5	91.3	899	10	US-09-970-944-2	Sequence 2, Appli
8	539	79.0	931	10	US-09-970-944-16	Sequence 16, Appl
9	539	79.0	931	10	US-09-970-944-17	Sequence 17, Appl
10	539	79.0	931	11	US-09-972-211-122	Sequence 122, App
11	539	79.0	931	11	US-09-972-211-125	Sequence 125, App
12	539	79.0	931	15	US-10-087-684-36	Sequence 36, Appl
13	539	79.0	931	15	US-10-218-779-36	Sequence 36, Appl
14	539	79.0	931	15	US-10-037-417-118	Sequence 118, App
15	539	79.0	931	15	US-10-037-417-119	Sequence 119, App
16	539	79.0	931	15	US-10-037-417-120	Sequence 120, App
17	539	79.0	931	15	US-10-096-625-122	Sequence 122, App
18	539	79.0	931	15	US-10-096-625-125	Sequence 125, App
19	531	77.9	931	10	US-09-970-944-15	Sequence 15, Appl
20	531	77.9	931	11	US-09-972-211-121	Sequence 121, App
21	531	77.9	931	15	US-10-087-684-35	Sequence 35, Appl
22	531	77.9	931	15	US-10-037-417-117	Sequence 117, App
23	531	77.9	931	15	US-10-096-625-121	Sequence 121, App
24	531	77.9	1010	15	US-10-218-779-35	Sequence 35, Appl
25	523	76.7	933	15	US-10-087-684-2	Sequence 2, Appli
26	523	76.7	933	15	US-10-087-684-4	Sequence 4, Appli
27	523	76.7	933	15	US-10-218-779-2	Sequence 2, Appli
28	523	76.7	933	15	US-10-218-779-4	Sequence 4, Appli
29	523	76.7	945	14	US-10-028-072-146	Sequence 146, App
30	523	76.7	945	14	US-10-140-808-146	Sequence 146, App
31	523	76.7	945	14	US-10-121-049-146	Sequence 146, App
32	523	76.7	945	14	US-10-123-904-146	Sequence 146, App
33	523	76.7	945	14	US-10-140-470-146	Sequence 146, App
34	523	76.7	945	14	US-10-175-746-146	Sequence 146, App
35	523	76.7	945	14	US-10-176-918-146	Sequence 146, App
36	523	76.7	945	14	US-10-176-921-146	Sequence 146, App
37	523	76.7	945	14	US-10-137-865-146	Sequence 146, App
38	523	76.7	945	14	US-10-140-474-146	Sequence 146, App
39	523	76.7	945	14	US-10-142-431-146	Sequence 146, App
40	523	76.7	945	14	US-10-143-114-146	Sequence 146, App
41	523	76.7	945	14	US-10-142-419-146	Sequence 146, App
42	523	76.7	945	14	US-10-123-262-146	Sequence 146, App
43	523	76.7	945	14	US-10-142-423-146	Sequence 146, App
44	523	76.7	945	14	US-10-121-050-146	Sequence 146, App
45	523	76.7	945	14	US-10-141-755-146	Sequence 146, App

ALIGNMENTS

RESULT 1

US-09-918-779-2

; Sequence 2, Application US/09918779

; Publication No. US20030064369A1

; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-779-2

Query Match 100.0%; Score 682; DB 10; Length 898;

Best Local Similarity 100.0%; Pred. No. 5.6e-53;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-10-624-932-2

; Sequence 2, Application US/10624932

; Publication No. US20040096877A1

; GENERAL INFORMATION:

; APPLICANT: Taupier, Raymond

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Rastelli, Luca

; APPLICANT: Spaderna, Steven

; APPLICANT: Shimkets, Richard

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Spytek, Kimberly

; APPLICANT: Shenoy, Suresh

; APPLICANT: Li, Li

; APPLICANT: Gusev, Vladimir

; APPLICANT: Grosse, William

; APPLICANT: Alsobrook, John

; APPLICANT: Lepley, Denise

; APPLICANT: Burgess, Catherine

; APPLICANT: Gerlach, Valerie

; APPLICANT: Ellerman, Karen

; APPLICANT: MacDougall, John

; APPLICANT: Stone, David

; APPLICANT: Smithson, Glennnda

; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-074 US

; CURRENT APPLICATION NUMBER: US/10/624,932

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: 09/918,779

; PRIOR FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 60/221,409

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 60/222,840

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,752

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,762

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,770

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,769

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/225,146

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/225,392


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Query Match          96.9%; Score 661; DB 14; Length 898;
Best Local Similarity 96.6%; Pred. No. 4.3e-51;
Matches 113; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Db 232 STSAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRCTNPAPLNGGAFCEGQNVOQTAC 291

Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDRNCTSDL 117
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Db 292 ATLCPVDGSWSSWSKWSACGLDCTHWSRECS DPAPRNGGEECRGADLDTRNCTSDL 348

US-10-240-154-16
; Sequence 16, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-240-154-16

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Query Match          96.9%;  Score 661;  DB 14;  Length 898;
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Matches 113;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;

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US-09-970-944-2
; Sequence 2, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A

```
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-944-2
```

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Query Match          91.3%; Score 622.5; DB 10; Length 899;
Best Local Similarity 92.4%; Pred. No. 1.2e-47;
Matches 109; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
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Qy      1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNV-QKTA 59
          ||||||||||||||||||||||||||||||||||||||||||||| :|
Db      232 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNVHDRTV 291

Qy      60 CATLCPVDGWSWPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDL 117
          : | |||||||||||||||||||||||||||||||||||||||||
Db      292 SLLVSV DGSWPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDL DTRNCTSDL 349
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RESULT 8

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US-09-970-944-16
; Sequence 16, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-970-944-16
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Query Match          79.0%; Score 539; DB 10; Length 931;
Best Local Similarity 73.5%; Pred. No. 4e-40;
Matches 86; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
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```
; Sequence 122, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
```

; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennnda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245Ael Human Proteins, Polynucleotides
Encoding Them And
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-122

Query Match 79.0%; Score 539; DB 11; Length 931;
Best Local Similarity 73.5%; Pred. No. 4e-40;
Matches 86; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTAC 60
| :| ||||| ||||| ||||| :| ||||| ||||| :| ||||| ||||| :| ||| ||
Db 250 STTATVIVYVNGGWSTWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIAC 309

Qy 61 ATLCPWDGWSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDRNCTSDL 117
||||| |:||||| || :|||| |||: |||: |||: |||: ||| :||| |
Db 310 TTLCPWDGRWTPWSKWSTCGTECTHWRRRECTAPAPKNGGKDCDGLVLQSKNCTDGL 366

RESULT 11

US-09-972-211-125

; Sequence 125, Application US/09972211

; Publication No. US20040048245A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard A

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Burgess, Catherine E

; APPLICANT: Zerhusen, Bryan D

; APPLICANT: Mezes, Peter S

; APPLICANT: Rastelli, Luca

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Grosse, William M

; APPLICANT: Alsobrook II, John P

; APPLICANT: Lepley, Denise M

; APPLICANT: Spytek, Kimberly Ann

; APPLICANT: Li, Li

; APPLICANT: Edinger, Shlomit

; APPLICANT: Gerlach, Valerie

; APPLICANT: Ellerman, Karen

; APPLICANT: MacDougall, John R

; APPLICANT: Gunther, Erik

; APPLICANT: Millet, Isabelle

; APPLICANT: Stone, David J

; APPLICANT: Smithson, Glennnda

; APPLICANT: Szekeres Jr, Edward S

; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides
Encoding Them And

; TITLE OF INVENTION: Methods Of Using The Same

; FILE REFERENCE: 21402-141

; CURRENT APPLICATION NUMBER: US/09/972,211

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,325

; PRIOR FILING DATE: 2000-10-05

; PRIOR APPLICATION NUMBER: 60/238,323

; PRIOR FILING DATE: 2000-10-05

; PRIOR APPLICATION NUMBER: 60/238,400

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/238,397

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/238,401

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/238,379

; PRIOR FILING DATE: 2000-10-06

US-10-037-417-118

; Sequence 118, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 931
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-037-417-118

Query Match 79.0%; Score 539; DB 15; Length 931;
Best Local Similarity 73.5%; Pred. No. 4e-40;
Matches 86; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

```
Qy      1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNVQKTAC 60
      | :| ||||| ||||| ||||| :: ||||:||||:|:||||| ||||| ||||| ||
Db      250 STTATVIVYVNGGWSTWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIAC 309

Qy      61 ATLCPWDGWSWPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRNCTSDL 117
      ||||| ||:||||| ||:||||| |||: |||:||||:| | | :||| |
Db      310 TTLCPVDGRWTPWSKWSTCGTECTHWRRRECTAPAPKNGGKDCDGLVLQSKNCTDGL 366
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RESULT 15

US-10-037-417-119

; Sequence 119, Application US/10037417
; Publication No. US20040052806A1

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-235

; CURRENT APPLICATION NUMBER: US/10/037,417

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,360

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411

; PRIOR FILING DATE: 2001-02-28

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; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-037-417-119
```

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Query Match          79.0%; Score 539; DB 15; Length 931;
Best Local Similarity 73.5%; Pred. No. 4e-40;
Matches 86; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
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Qy      1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 60
      | :| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      250 STTATVIVYVNGGWSTWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIAC 309

Qy      61 ATLCPPVDGSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTNRCTSDL 117
      ||||| | :||| | | :||| | || : ||| :||| :||| :||| :||| |
Db      310 TTLCPPVDGRWTPWSKWSTCGTECTHWRRRECTAPAPKNGGKDCDGLVLQSKNCTDGL 366
```

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Search completed: March 1, 2005, 09:51:30
Job time : 23.5184 secs
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:41:47 ; Search time 21.4031 Seconds
 (without alignments)
 2799.282 Million cell updates/sec

Title: US-10-624-932-2_COPY_232_348
 Perfect score: 682
 Sequence: 1 SASAAVIVYVNGGWSTWTEW.....NGGEECQGTDLDTNRNCTSDL 117

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	673	98.7	898	1	UN5A_MOUSE	Q8kls4 mus musculu
2	661	96.9	898	1	UN5A_RAT	O08721 rattus norv
3	539	79.0	931	1	UN5C_HUMAN	O95185 homo sapien
4	534	78.3	931	1	UN5C_CHICK	Q7t2z5 gallus gall
5	531	77.9	931	1	UN5C_MOUSE	O08747 mus musculu
6	526	77.1	931	1	UN5C_RAT	Q761x5 rattus norv
7	523	76.7	945	1	UN5B_HUMAN	Q8izj1 homo sapien
8	522	76.5	945	1	UN5B_MOUSE	Q8kls3 mus musculu
9	522	76.5	945	1	UN5B_RAT	O08722 rattus norv
10	502	73.6	943	1	UN5B_XENLA	Q8jgt4 xenopus lae
11	485	71.1	953	1	UN5D_HUMAN	Q6uxz4 homo sapien
12	484	71.0	956	1	UN5D_MOUSE	Q8kls2 mus musculu
13	322	47.2	842	1	UN5A_HUMAN	Q6zn44 homo sapien
14	315	46.2	2673	2	Q96SC3	Q96sc3 homo sapien
15	314	46.0	1244	2	Q69YJ3	Q69yj3 homo sapien

16	314	46.0	5636	2	Q96RW7	Q96rw7 homo sapien
17	303	44.4	919	1	UNC5_CAEEL	Q26261 caenorhabdi
18	284	41.6	1074	1	SM5A_HUMAN	Q13591 homo sapien
19	280	41.1	1077	1	SM5A_MOUSE	Q62217 mus musculu
20	277.5	40.7	1081	2	Q9U631	Q9u631 drosophila
21	277.5	40.7	1091	2	Q7YU67	Q7yu67 drosophila
22	277.5	40.7	1093	2	Q9VTT0	Q9vtt0 drosophila
23	274	40.2	1170	1	TSP2_BOVIN	Q95116 bos taurus
24	271	39.7	1172	1	TSP2_MOUSE	Q03350 mus musculu
25	271	39.7	1172	2	Q7TMT3	Q7tmt3 mus musculu
26	271	39.7	1172	2	Q8CG21	Q8cg21 mus musculu
27	271	39.7	1388	2	Q7QKD0	Q7qkd0 anopheles g
28	269.5	39.5	1072	1	UNC5_DROME	Q95tu8 drosophila
29	269.5	39.5	1584	1	BAI1_HUMAN	O14514 homo sapien
30	269	39.4	1088	2	Q6PCK8	Q6pck8 xenopus lae
31	268	39.3	1522	1	BAI3_HUMAN	O60242 homo sapien
32	267	39.1	612	2	Q6ZQ96	Q6zq96 mus musculu
33	267	39.1	1282	2	Q68FL1	Q68fl1 mus musculu
34	267	39.1	1522	1	BAI3_MOUSE	Q80zf8 mus musculu
35	266	39.0	1172	1	TSP2_HUMAN	P35442 homo sapien
36	265.5	38.9	1582	2	Q8CGM0	Q8cgm0 mus musculu
37	263	38.6	1092	2	Q6UY12	Q6uy12 homo sapien
38	261.5	38.3	1093	1	SM5B_HUMAN	Q9p283 homo sapien
39	261.5	38.3	1151	2	Q6DD89	Q6dd89 homo sapien
40	261	38.3	478	2	Q8BVE5	Q8bve5 m mus muscu
41	261	38.3	632	2	Q6ZPQ8	Q6zpq8 mus musculu
42	261	38.3	1093	1	SM5B_MOUSE	Q60519 mus musculu
43	261	38.3	1122	2	Q7TT33	Q7tt33 mus musculu
44	261	38.3	1170	2	Q71SA3	Q7lsa3 rattus norv
45	258	37.8	1170	1	TSP1_HUMAN	P07996 homo sapien

ALIGNMENTS

RESULT 1

UN5A_MOUSE

ID UN5A_MOUSE STANDARD; PRT; 898 AA.
 AC Q8KLS4; Q6PEF7; Q80T71;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
 GN Name=Unc5a; Synonyms=Kiaa1976, Unc5h1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse unc-5 genes and their expression patterns at
 RT mid-gestation."
 RL Mech. Dev. 118:191-197(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 3).

RC TISSUE=Brain;
 RX MEDLINE=22579291; PubMed=12693553;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
 RA Nakajima D., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:35-48(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q8K1S4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8K1S4-2; Sequence=VSP_011697;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q8K1S4-3; Sequence=VSP_011696;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Restricted to central nervous system.

CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
CC participates in the induction of apoptosis (By similarity).
CC -!- PTM: Phosphorylated by PKC in vitro. Phosphorylated on cytoplasmic
CC tyrosine residues (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ487852; CAD32250.1; -.
DR EMBL; AK122575; BAC65857.1; ALT_INIT.
DR EMBL; BC058084; AAH58084.1; -.
DR HSSP; P07996; 1LSL.
DR MGD; MGI:894682; Unc5a.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 898 Netrin receptor UNC5A.
FT DOMAIN 26 361 Extracellular (Potential).
FT TRANSMEM 362 382 Potential.
FT DOMAIN 383 898 Cytoplasmic (Potential).
FT DOMAIN 44 141 Ig-like.
FT DOMAIN 155 234 Ig-like C2-type.

FT	DOMAIN	242	296	TSP type-1 1.
FT	DOMAIN	298	350	TSP type-1 2.
FT	DOMAIN	495	598	ZU5.
FT	DOMAIN	817	897	Death.
FT	SITE	396	397	Cleavage (by caspase-3) (By similarity).
FT	SITE	661	679	Interaction with DCC (By similarity).
FT	DISULFID	65	124	By similarity.
FT	DISULFID	170	221	By similarity.
FT	CARBOHYD	107	107	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	218	218	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	343	343	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	1	790	Missing (in isoform 3).
FT				/FTId=VSP_011696.
FT	VARSPLIC	241	296	Missing (in isoform 2).
FT				/FTId=VSP_011697.
FT	CONFLICT	217	217	A -> P (in Ref. 3).
SQ	SEQUENCE	898 AA;	98856 MW;	59F04BA2E196C1DB CRC64;

Query Match 98.7%; Score 673; DB 1; Length 898;
 Best Local Similarity 98.3%; Pred. No. 3.9e-55;
 Matches 115; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTAC	60
Db	232	SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTAC	291
Qy	61	ATLCPVDGSWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDL DTRNCTSDL	117
Db	292	ATLCPVDGSWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECRGADLDTRNCTSDL	348

RESULT 2

UN5A_RAT

ID UN5A_RAT STANDARD; PRT; 898 AA.
 AC 008721;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
 GN Name=Unc5a; Synonyms=Unc5h1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Ventral spinal cord;
 RX MEDLINE=97271897; PubMed=9126742;
 RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
 RA Tessier-Lavigne M.;
 RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
 RT receptors.";
 RL Nature 386:833-838(1997).
 RN [2]
 RP FUNCTION, AND INTERACTION WITH DCC.
 RX PubMed=10399920;

RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
 RA Stein E.;
 RT "A ligand-gated association between cytoplasmic domains of UNC5 and
 RT DCC family receptors converts netrin-induced growth cone attraction to
 RT repulsion.";
 RL Cell 97:927-941(1999).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX PubMed=11472849;
 RA Barrett C., Guthrie S.;
 RT "Expression patterns of the netrin receptor UNC5H1 among developing
 RT motor neurons in the embryonic rat hindbrain.";
 RL Mech. Dev. 106:163-166(2001).
 RN [4]
 RP FUNCTION.
 RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
 RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
 RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
 RL EMBO J. 20:2715-2722(2001).
 RN [5]
 RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH MAGED1.
 RX PubMed=12598531; DOI=10.1074/jbc.M300415200;
 RA Williams M.E., Strickland P., Watanabe K., Hinck L.;
 RT "UNC5H1 induces apoptosis via its juxtamembrane region through an
 RT interaction with NRAGE.";
 RL J. Biol. Chem. 278:17483-17490(2003).
 RN [6]
 RP INTERACTION WITH PRKCABP, PHOSPHORYLATION, AND MUTAGENESIS OF
 RP 896-ALA--CYS-898.
 RX PubMed=14672991; DOI=23/36/11279;
 RA Williams M.E., Wu S.C.-Y., McKenna W.L., Hinck L.;
 RT "Surface expression of the netrin receptor UNC5H1 is regulated through
 RT a protein kinase C-interacting protein/protein kinase-dependent
 RT mechanism.";
 RL J. Neurosci. 23:11279-11288(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Expressed at early stages of neural tube development in
 CC the ventral spinal cord. In developing hindbrain, it colocalizes
 CC with a number of cranial motor neuron subpopulations from
 CC embryonic E11 to E14, while DCC is expressed by motor neurons at
 CC E12. Also expressed in non-neural structures, such as the basal
 CC plane of the hindbrain and midbrain, in the developing
 CC hypothalamus, thalamus and in the pallidum.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis.

CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity). Phosphorylated by PKC in vitro.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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 CC -----

DR EMBL; U87305; AAB57678.1; -.
 DR HSSP; P07996; 1LSL.
 DR RGD; 621755; Unc5h1.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.

KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.

FT	SIGNAL	1	25	Potential.
FT	CHAIN	26	898	Netrin receptor UNC5A.
FT	DOMAIN	26	361	Extracellular (Potential).
FT	TRANSMEM	362	382	Potential.
FT	DOMAIN	383	898	Cytoplasmic (Potential).
FT	DOMAIN	44	141	Ig-like.
FT	DOMAIN	155	238	Ig-like C2-type.
FT	DOMAIN	242	296	TSP type-1 1.
FT	DOMAIN	298	350	TSP type-1 2.
FT	DOMAIN	495	598	ZU5.
FT	DOMAIN	817	897	Death.
FT	SITE	396	397	Cleavage (by caspase-3) (By similarity).

FT	SITE	661	679	Interaction with DCC (By similarity).
FT	DISULFID	65	124	By similarity.
FT	DISULFID	170	221	By similarity.
FT	CARBOHYD	107	107	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	218	218	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	343	343	N-linked (GlcNAc. . .) (Potential).
FT	MUTAGEN	896	898	Missing: Abolishes interaction with
FT				PRKCABP.
SQ	SEQUENCE	898 AA;	98840 MW;	7A3CBCB9E7ACA135 CRC64;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNAPLNGGAFCEGQNVOQTAC 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 232 STSAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNAPLNGGAFCEGQNVOQTAC 291

Qy 61 ATLCVPDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDTRNCTSDL 117
| | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | |
Db 292 ATLCVPDGSWSSWSKWSACGLDCTHWSRECS DPAPRNGGEECRGADLDTRNCTSDL 348

RESULT 3

```

ID      UN5C HUMAN          STANDARD;          PRT;      931 AA.
AC      O95185; Q8IUT0;
DT      25-OCT-2004 (Rel. 45, Created)
DT      25-OCT-2004 (Rel. 45, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).
GN      Name=UNC5C; Synonyms=UNC5H3;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC      TISSUE=Brain;
RX      MEDLINE=99000841; PubMed=9782087; DOI=10.1006/geno.1998.5425;
RA      Ackerman S.L., Knowles B.B.;
RT      "Cloning and mapping of the UNC5C gene to human chromosome 4q21-q23.";
RL      Genomics 52:205-208(1998).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM 2).
RC      TISSUE=Lung;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O95185-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O95185-2; Sequence=VSP_011700, VSP_011701;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
 CC kidney. Not expressed in developing or adult lung.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by
 CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----

DR EMBL; AF055634; AAC67491.1; -.
 DR EMBL; BC041156; AAH41156.1; -.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:12569; UNC5C.
 DR MIM; 603610; -.
 DR GO; GO:0005042; F:netrin receptor activity; TAS.
 DR GO; GO:0007411; P:axon guidance; TAS.
 DR GO; GO:0007420; P:brain development; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 931 Netrin receptor UNC5C.
 FT DOMAIN 41 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).
 FT SITE 694 712 Interaction with DCC (By similarity).
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT MOD_RES 568 568 Phosphotyrosine (By similarity).
 FT CARBOHYD 236 236 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc . . .) (Potential).
 FT VARSPLIC 370 370 T -> SFIYPISTEQRTQNEYGFSS (in isoform 2).
 FT /FTid=VSP_011700.

FT	VARSPLIC	579	931	Missing (in isoform 2).
FT				/FTId=VSP_011701.
FT	VARIANT	37	37	G -> V (in dbSNP:2306715).
FT				/FTId=VAR_019731.
FT	VARIANT	721	721	T -> M (in dbSNP:2289043).
FT				/FTId=VAR_019732.
FT	CONFLICT	219	219	T -> I (in Ref. 1).
FT	CONFLICT	489	489	S -> T (in Ref. 1).
SQ	SEQUENCE	931 AA;	103101 MW;	EFD71122C98DABB8 CRC64;

```

Qy      1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTAC 60
      | :| ||||| ||||| ||||| :| ||| :||| :| :| ||||| ||||| :||| ||
Db      250 STTATVIVYVNGGWSTWTEWSVCNSRCGRGYQKRTTCTNPAPLNGGAFCEGQSVQKIAC 309

Qy      61 ATLCVPDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDL 117
      ||||| ||||| :||| :||| :||| :||| :| | | :||| |
Db      310 TTLCPVDGRWTFWSKWSTCGTECTHWRRRECTAPAPKNGGKDCDGLVLOSKNCTDGL 366

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RESULT 4

```

ID      UN5C_CHICK      STANDARD;      PRT;      931 AA.
AC      Q7T2Z5;
DT      25-OCT-2004 (Rel. 45, Created)
DT      25-OCT-2004 (Rel. 45, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
DE      (cUNC-5H3).
GN      Name=UNC5C;
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX      PubMed=12799087;
RA      Guan W., Condic M.L.;
RT      "Characterization of Netrin-1, Neogenin and cUNC-5H3 expression during
RT      chick dorsal root ganglia development.";
RL      Gene Expr. Patterns 3:369-373(2003).
CC      -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC      axon repulsion of neuronal growth cones in the developing nervous
CC      system upon ligand binding (By similarity).
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -!- TISSUE SPECIFICITY: Restricted to proprioceptive neurons.
CC      -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC      similarity).
CC      -!- SIMILARITY: Belongs to the UNC-5 family.
CC      -!- SIMILARITY: Contains 1 death domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC      -!- SIMILARITY: Contains 2 TSP type-1 domains.

```

CC -!- SIMILARITY: Contains 1 ZU5 domain.

```

DR      EMBL; AY187310; AAO67275.1; -.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR000884; TSP1.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00531; Death; 1.
DR      Pfam; PF00047; ig; 1.
DR      Pfam; PF00090; TSP_1; 2.
DR      Pfam; PF00791; ZU5; 1.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00408; IGc2; 1.
DR      SMART; SM00209; TSP1; 2.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR      PROSITE; PS50835; IG_LIKE; 1.
DR      PROSITE; PS50092; TSP1; 2.
KW      Developmental protein; Immunoglobulin domain; Phosphorylation;
KW      Receptor; Repeat; Signal; Transmembrane.
FT      SIGNAL      1      39      Potential.
FT      CHAIN        40      931      Netrin receptor UNC5C.
FT      DOMAIN       40      380      Extracellular (Potential).
FT      TRANSMEM     381      401      Potential.
FT      DOMAIN       402      931      Cytoplasmic (Potential).
FT      DOMAIN       62      159      Ig-like.
FT      DOMAIN       161      256      Ig-like C2-type.
FT      DOMAIN       260      314      TSP type-1 1.
FT      DOMAIN       316      368      TSP type-1 2.
FT      DOMAIN       528      631      ZU5.
FT      DOMAIN       850      929      Death.
FT      DISULFID     83      142      By similarity.
FT      DISULFID     188      239      By similarity.
FT      CARBOHYD     236      236      N-linked (GlcNAc . . .) (Potential
FT      CARBOHYD     361      361      N-linked (GlcNAc . . .) (Potential
SQ      SEQUENCE     931 AA;  102906 MW;  1E23A0D84F2E2C62 CRC64;

```

RESULT 5

UN5C_MOUSE

ID UN5C_MOUSE STANDARD; PRT; 931 AA.
AC 008747; Q8CD16;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
DE (Rostral cerebellar malformation protein).
GN Name=Unc5c; Synonyms=Rcm, Unc5h3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, DISEASE, AND TISSUE
RP SPECIFICITY.
RC STRAIN=C57B6/SJL;
RX MEDLINE=97271898; PubMed=9126743;
RA Ackerman S.L., Kozak L.P., Przyborski S.A., Rund L.A., Boyer B.B.,
RA Knowles B.B.;
RT "The mouse rostral cerebellar malformation gene encodes an UNC-5-like
RT protein.";
RL Nature 386:838-842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX PubMed=9389662;
 RA Przyborski S.A., Knowles B.B., Ackerman S.L.;
 RT "Embryonic phenotype of Unc5h3 mutant mice suggests chemorepulsion
 RT during the formation of the rostral cerebellar boundary.";
 RL Development 125:41-50(1998).
 RN [4]
 RP INTERACTION WITH DCC.
 RX PubMed=10399920;
 RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
 RA Stein E.;
 RT "A ligand-gated association between cytoplasmic domains of UNC5 and
 RT DCC family receptors converts netrin-induced growth cone attraction to
 RT repulsion.";
 RL Cell 97:927-941(1999).
 RN [5]
 RP PHOSPHORYLATION SITE TYR-568, AND MUTAGENESIS OF TYR-568.
 RX PubMed=11533026; DOI=10.1074/jbc.M103872200;
 RA Tong J., Killeen M., Steven R., Binns K.L., Culotti J., Pawson T.;
 RT "Netrin stimulates tyrosine phosphorylation of the UNC-5 family of
 RT netrin receptors and induces Shp2 binding to the RCM cytodomain.";
 RL J. Biol. Chem. 276:40917-40925(2001).
 RN [6]
 RP FUNCTION.
 RX PubMed=12451134; DOI=22/23/10346;
 RA Finger J.H., Bronson R.T., Harris B., Johnson K., Przyborski S.A.,
 RA Ackerman S.L.;
 RT "The netrin 1 receptors Unc5h3 and Dcc are necessary at multiple
 RT choice points for the guidance of corticospinal tract axons.";
 RL J. Neurosci. 22:10346-10356(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=008747-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=008747-2; Sequence=VSP_011702;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Highly expressed in brain and lung. Weakly expressed in
 CC testis, ovary, spleen, thymus and bladder. Expressed at very low
 CC level in kidney, intestine and salivary gland.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by
 CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is

CC netrin-dependent.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- DISEASE: Defects in Unc5c are the cause of rostral cerebellar
 CC malformation (Rcm). Rcm is characterized by cerebellar and
 CC midbrain defects, apparently as a result of abnormal neuronal
 CC migration.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; U72634; AAB54103.1; -.
 DR EMBL; AK031655; BAC27495.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:1095412; Unc5c.
 DR GO; GO:0005886; C:plasma membrane; IC.
 DR GO; GO:0005042; F:netrin receptor activity; IDA.
 DR GO; GO:0005515; F:protein binding; IDA.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0030334; P:regulation of cell migration; IMP.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 931 Netrin receptor UNC5C.

RT caused by mutations in the netrin-1 receptor gene Unc5h3.";
 RL Brain Res. Mol. Brain Res. 122:103-108(2004).
 RN [2]
 RP FUNCTION.
 RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
 RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
 RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
 RL EMBO J. 20:2715-2722(2001).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
 CC kidney. Not expressed in developing or adult lung.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by
 CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- DISEASE: Defects in Unc5c are the cause of cerebellar vermis
 CC defect (cvd) and hobble (hob) phenotypes. Cvd and hob rats exhibit
 CC cerebellar and midbrain defects, possibly as a result of abnormal
 CC neuronal migration, and exhibit laminar structure abnormalities in
 CC the fused cerebellar hemispheres and ectopic cerebellar tissues in
 CC the cerebello-pontine junction.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AB118026; BAD05181.1; -.
 DR RGD; 735109; Unc5c.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.


```

DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR008085; TSP_1.
DR   InterPro; IPR000906; ZU5.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00090; TSP_1; 2.
DR   Pfam; PF00791; ZU5; 1.
DR   PRINTS; PR01705; TSP1REPEAT.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00209; TSP1; 2.
DR   SMART; SM00218; ZU5; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS50092; TSP1; 2.
KW   Apoptosis; Developmental protein; Immunoglobulin domain;
KW   Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
FT   SIGNAL             1         40         Potential.
FT   CHAIN              41        931        Netrin receptor UNC5C.
FT   DOMAIN            41        380        Extracellular (Potential).
FT   TRANSMEM          381        401        Potential.
FT   DOMAIN            402        931        Cytoplasmic (Potential).
FT   DOMAIN            62        159        Ig-like.
FT   DOMAIN            161       256        Ig-like C2-type.
FT   DOMAIN            260       314        TSP type-1 1.
FT   DOMAIN            316       368        TSP type-1 2.
FT   DOMAIN            528       631        ZU5.
FT   DOMAIN            850       929        Death.
FT   SITE              415       416        Cleavage (by caspase-3) (By similarity).
FT   SITE              694       712        Interaction with DCC (By similarity).
FT   DISULFID          83        142        By similarity.
FT   DISULFID          188       239        By similarity.
FT   MOD_RES           568       568        Phosphotyrosine (By similarity).
FT   CARBOHYD          236       236        N-linked (GlcNAc . . .) (Potential).
FT   CARBOHYD          361       361        N-linked (GlcNAc . . .) (Potential).
SQ   SEQUENCE          931 AA; 103134 MW; 25B183A97BCB8401 CRC64;

```

Query Match 77.1%; Score 526; DB 1; Length 931;
Best Local Similarity 71.8%; Pred. No. 3e-41;
Matches 84; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

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Qy      1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCNPNAPLNGGAFCEGQNVQKTAC 60
      | :| ||||| ||||| ||||| :| ||| :||| :| :| ||||| ||||| :||| ||
Db      250 STTATVIVYVNGGWSTWAEWSVCNSRCGRGYQKRTRTCTNPNAPLNGGAFCEGQSVQKIAC 309
      .
Qy      61 ATLCVPDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDL 117
      ||||| | :| ||||| :| ||||| ||| :||| :||| :| | | :||| |
Db      310 TTLCPVDGRWTSWSKWSTCGTECTHWRRRECTAPAPKNGGKDCDGLVLOSKNCTDGL 366

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RESULT 7

UN5B HUMAN

ID UN5B HUMAN STANDARD: PRT: 945 AA.

AC Q8IZJ1; Q86SN3; Q8N1Y2; Q9H9F3;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2)
 DE (p53-regulated receptor for death and life protein 1)
 DE (UNQ1883/PRO4326).
 GN Name=UNC5B; Synonyms=P53RDL1, UNC5H2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION
 RP WITH GNAI2.
 RC TISSUE=Lung;
 RX MEDLINE=22246081; PubMed=12359238; DOI=10.1016/S0006-291X(02)02277-5;
 RA Komatsuzaki K., Dalvin S., Kinane T.B.;
 RT "Modulation of G(ialpha(2)) signaling by the axonal guidance molecule
 RT UNC5H2.";
 RL Biochem. Biophys. Res. Commun. 297:898-905(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND MUTAGENESIS OF ASP-412.
 RX PubMed=12598906; DOI=10.1038/ncb943;
 RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
 RT "p53RDL1 regulates of p53-dependent apoptosis.";
 RL Nat. Cell Biol. 5:216-223(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [4]
 RP SEQUENCE OF 361-945 FROM N.A.
 RC TISSUE=Amygdala, and Teratocarcinoma;
 RX PubMed=14702039; DOI=10.1038/ngl285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiuji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [5]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity). Interacts with GNAI2 via its cytoplasmic part.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8IZJ1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8IZJ1-2; Sequence=VSP_011698;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed at
 CC lower level in developing lung, cartilage, kidney and
 CC hematopoietic and immune tissues.
 CC -!- INDUCTION: By p53/TP53....
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.

```

CC  -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC  -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC  -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC  -!- SIMILARITY: Contains 1 ZU5 domain.
CC  -----
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CC  -----
DR  EMBL; AY126437; AAM95701.1; -.
DR  EMBL; AB096256; BAC57998.1; -.
DR  EMBL; AY358351; AAQ88717.1; -.
DR  EMBL; AK022859; BAB14276.1; ALT_INIT.
DR  EMBL; AK094595; BAC04382.1; ALT_INIT.
DR  HSSP; P07996; 1LSL.
DR  Genew; HGNC:12568; UNC5B.
DR  MIM; 607870; -.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR011029; DEATH like.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003598; Ig_c2.
DR  InterPro; IPR000884; TSP1.
DR  InterPro; IPR008085; TSP_1.
DR  InterPro; IPR000906; ZU5.
DR  Pfam; PF00531; Death; 1.
DR  Pfam; PF00047; ig; 1.
DR  Pfam; PF00090; TSP_1; 2.
DR  Pfam; PF00791; ZU5; 1.
DR  PRINTS; PR01705; TSP1REPEAT.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00408; IGc2; 1.
DR  SMART; SM00209; TSP1; 2.
DR  SMART; SM00218; ZU5; 1.
DR  PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR  PROSITE; PS50835; IG_LIKE; 1.
DR  PROSITE; PS50092; TSP1; 2.
KW  Alternative splicing; Apoptosis; Developmental protein;
KW  Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
KW  Repeat; Signal; Transmembrane.
FT  SIGNAL      1      26      Potential.
FT  CHAIN       27     945     Netrin receptor UNC5B.
FT  DOMAIN      27     377     Extracellular.(Potential).
FT  TRANSMEM    378     398     Potential.
FT  DOMAIN      399     945     Cytoplasmic (Potential).
FT  DOMAIN      48      145     Ig-like.
FT  DOMAIN     147     242     Ig-like C2-type.
FT  DOMAIN     246     300     TSP type-1 1.
FT  DOMAIN     302     354     TSP type-1 2.
FT  DOMAIN     541     644     ZU5.
FT  DOMAIN     865     943     Death.
FT  SITE        412     413     Cleavage (by caspase-3).
FT  SITE        707     725     Interaction with DCC (By similarity).
FT  DISULFID     69     128     By similarity.

```

FT	DISULFID	174	225	By similarity.
FT	CARBOHYD	222	222	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	347	347	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	356	367	NKKTLSDPNSHL -> M (in isoform 2).
FT				/FTId=VSP_011698.
FT	VARIANT	516	516	A -> T (in dbSNP:10509332).
FT				/FTId=VAR_019730.
FT	MUTAGEN	412	412	D->N: Abolishes cleavage by caspase-3 and
FT				subsequent induction of apoptosis.
FT	CONFLICT	483	483	K -> E (in Ref. 3).
FT	CONFLICT	851	851	L -> P (in Ref. 3; BAB14276).
SQ	SEQUENCE	945 AA;	103637 MW;	56064E335F323447 CRC64;

Query Match 76.7%; Score 523; DB 1; Length 945;
 Best Local Similarity 71.8%; Pred. No. 5.8e-41;
 Matches 84; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy	1	SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC	60
		: : : :	
Db	236	STTATVIVYVNGGWSSWAIEWSPCSNRCGRGWQKRTCTNPAPLNGGAFCEGQAFQKTAC	295
Qy	61	ATLCPVDGSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDRNCTSDL	117
		: : : : : :	
Db	296	TTICPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGL	352

RESULT 8

UN5B_MOUSE

ID UN5B_MOUSE STANDARD; PRT; 945 AA.
 AC Q8K1S3; Q6PFH0; Q80Y85; Q9D398;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
 GN Name=Unc5b; Synonyms=Unc5h2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse unc-5 genes and their expression patterns at
 RT mid-gestation.";
 RL Mech. Dev. 118:191-197(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteu G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX PubMed=12799072;
 RA Dalvin S., Anselmo M.A., Prodhan P., Komatsuzaki K., Schnitzer J.J.,
 RA Kinane T.B.;
 RT "Expression of Netrin-1 and its two receptors DCC and UNC5H2 in the
 RT developing mouse lung.";
 RL Gene Expr. Patterns 3:279-283(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be

CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with GNAI2 via its cytoplasmic part (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8K1S3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8K1S3-2; Sequence=VSP_011699;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Expressed in lung
 CC during late development. Expressed during early blood vessel
 CC formation, in the semicircular canal and in a dorsal to ventral
 CC gradient in the retina.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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 CC -----

DR EMBL; AJ487853; CAD32251.1; -.
 DR EMBL; AK018177; BAB31108.1; -.
 DR EMBL; BC048162; AAH48162.1; ALT_INIT.
 DR EMBL; BC057560; AAH57560.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:894703; Unc5b.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.

DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 945 Netrin receptor UNC5B.
 FT DOMAIN 27 377 Extracellular (Potential).
 FT TRANSMEM 378 398 Potential.
 FT DOMAIN 399 945 Cytoplasmic (Potential).
 FT DOMAIN 48 145 Ig-like.
 FT DOMAIN 153 242 Ig-like C2-type.
 FT DOMAIN 246 300 TSP type-1 1.
 FT DOMAIN 302 354 TSP type-1 2.
 FT DOMAIN 541 644 ZU5.
 FT DOMAIN 865 943 Death.
 FT SITE 412 413 Cleavage (by caspase-3) (By similarity).
 FT SITE 707 725 Interaction with DCC (By similarity).
 FT DISULFID 69 128 By similarity.
 FT DISULFID 174 225 By similarity.
 FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 356 367 NQRTLNDPKSHP -> T (in isoform 2).
 FT /FTId=VSP_011699.
 FT CONFLICT 238 238 T -> A (in Ref. 2).
 FT CONFLICT 394 394 V -> E (in Ref. 2).
 FT CONFLICT 679 679 T -> S (in Ref. 2).
 FT CONFLICT 874 874 N -> D (in Ref. 2).
 SQ SEQUENCE 945 AA; 103738 MW; 80E896F0F0E06012 CRC64;

Query Match 76.5%; Score 522; DB 1; Length 945;
 Best Local Similarity 71.8%; Pred. No. 7.1e-41;
 Matches 84; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTAC 60
 | :| ||||| :| ||| || ||||| :| :||| ||||| |||||
 Db 236 STTATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTTRCTNPAPLNGGAFCEGQAFQKTAC 295
 Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDLDRNCTSDL 117
 | :||| :| :||| ||| :| ||||| | :||| :| || ||| :||| |
 Db 296 TTVCVPDGAWTEWSKWSACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGL 352

RESULT 9

UN5B_RAT

ID UN5B_RAT STANDARD; PRT; 945 AA.
 AC 008722;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
 GN Name=Unc5b; Synonyms=Unc5h2;
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RX MEDLINE=97271897; PubMed=9126742;
 RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
 RA Tessier-Lavigne M.;
 RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
 RT receptors.";
 RL Nature 386:833-838(1997).
 RN [2]
 RP FUNCTION, AND INTERACTION WITH DCC.
 RX PubMed=10399920;
 RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
 RA Stein E.;
 RT "A ligand-gated association between cytoplasmic domains of UNC5 and
 RT DCC family receptors converts netrin-induced growth cone attraction to
 RT repulsion.";
 RL Cell 97:927-941(1999).
 RN [3]
 RP FUNCTION, AND MUTAGENESIS OF ASP-412.
 RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
 RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
 RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
 RL EMBO J. 20:2715-2722(2001).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with GNAI2 via its cytoplasmic part (By
 CC similarity). Interacts with the cytoplasmic part of DCC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Expressed in the developing sensory ganglia that flank
 CC the spinal cord from E12, peaking at E14. Expressed in the roof
 CC plate region of the spinal cord from E14.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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DR EMBL; U87306; AAB57679.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621756; Unc5h2.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Apoptosis; Developmental protein; Immunoglobulin domain;
KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 945 Netrin receptor UNC5B.
FT DOMAIN 27 377 Extracellular (Potential).
FT TRANSMEM 378 398 Potential.
FT DOMAIN 399 945 Cytoplasmic (Potential).
FT DOMAIN 48 145 Ig-like.
FT DOMAIN 153 242 Ig-like C2-type.
FT DOMAIN 246 300 TSP type-1 1.
FT DOMAIN 302 354 TSP type-1 2.
FT DOMAIN 541 644 ZU5.
FT DOMAIN 865 943 Death.
FT SITE 412 413 Cleavage (by caspase-3).
FT SITE 707 725 Interaction with DCC.
FT DISULFID 69 128 By similarity.
FT DISULFID 174 225 By similarity.
FT CARBOHYD 222 222 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 347 347 N-linked (GlcNAc . . .) (Potential).
FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and
FT subsequent induction of apoptosis.
SQ SEQUENCE 945 AA; 103520 MW; 6E9C2A262E560B9B CRC64;

Query Match 76.5%; Score 522; DB 1; Length 945;
Best Local Similarity 71.8%; Pred. No. 7.1e-41;
Matches 84; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSC TNPAPLNGGAFCEGQNVQKTAC 60
| :| ||||| :| ||| || ||||| :| :||| |||||
Db 236 STTATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQACQKTAC 295

Qy 61 ATLCVPDGSWSPWSKWSACGLDCTHWSRECS DPAPRNGGEECQGTDLDTNRCTSDL 117
 Db 296 TTVCPVDGAWTEWSKWSACSTECAHWSRECMAPPPQNGGRDCSGTLLDSKNCTDGL 352

RESULT 10

UN5B_XENLA

ID UN5B_XENLA STANDARD; PRT; 943 AA.
 AC Q8JGT4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (UNC-5 homolog) (Protein XUNC-5).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=22239703; PubMed=12351179; DOI=10.1016/S0925-4773(02)00215-0;
 RA Anderson R.B., Holt C.E.;
 RT "Expression of UNC-5 in the developing Xenopus visual system.";
 RL Mech. Dev. 118:157-160(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: In the developing visual system, it is
 CC expressed within the developing optic vesicles and later become
 CC restricted to the dorsal ciliary marginal zone, a site of
 CC retinoblast proliferation and differentiation.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AY099459; AAM34486.1; -.
 DR HSSP; P07996; 1LSL.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.

DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Developmental protein; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 943 Netrin receptor UNC5B.
 FT DOMAIN 31 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 943 Cytoplasmic (Potential).
 FT DOMAIN 51 148 Ig-like.
 FT DOMAIN 150 245 Ig-like C2-type.
 FT DOMAIN 249 303 TSP type-1 1.
 FT DOMAIN 305 357 TSP type-1 2.
 FT DOMAIN 540 643 ZU5.
 FT DOMAIN 863 941 Death.
 FT DISULFID 72 131 By similarity.
 FT DISULFID 177 228 By similarity.
 FT CARBOHYD 225 225 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 350 350 N-linked (GlcNAc . .) (Potential).
 SQ SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175 CRC64;

Query Match 73.6%; Score 502; DB 1; Length 943;
 Best Local Similarity 67.5%; Pred. No. 5.5e-39;
 Matches 79; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

Qy 1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCSTNPAPLNGGAFCEGQNVQKTAC 60
 | :| |||:|||||:|||| | : || |||||:|:||||||| |||| || ||
 Db 239 STTATVIVFVNGGWSSWTEWSPCNNRCGHGWQKRTRTCTNPAPLNGGTMCEGQQYQKFAC 298

 Qy 61 ATLCPVDGSWSPWSKWSACGLDCTHWRSRECS DPAPRNGGEECQGTDL DTRNCTSDL 117
 |:|||| | : |||||| :|||||||: | |:|:|:| | ||:| | |
 Db 299 NTMCPVDGGWTEWSKWSACSTECTHWRSRECNAPTPKNGGKDCSGMLLD SKNCTDGL 355

RESULT 11

UN5D_HUMAN

ID UN5D_HUMAN STANDARD; PRT; 953 AA.
 AC Q6UXZ4; Q8WYP7;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4)
 DE (UNQ6012/PRO34692).
 GN Name=UNC5D; Synonyms=KIAA1777, UNC5H4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RA Nakajima D., Nakayama M., Nagase T., Ohara O.;
 RT "Identification of unc5H4 gene.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Receptor for netrin. May be involved in axon guidance by
 CC mediating axon repulsion of neuronal growth cones in the
 CC developing nervous system upon ligand binding. Axon repulsion in
 CC growth cones may be caused by its association with DCC that may
 CC trigger signaling for repulsion. It also acts as a dependence
 CC receptor required for apoptosis induction when not associated with
 CC netrin ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q6UXZ4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q6UXZ4-2; Sequence=VSP_011703;
 CC Note=No experimental confirmation available;
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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```

DR -----
DR EMBL; AB055056; BAB83663.1; -.
DR EMBL; AY358147; AAQ88514.1; -.
DR HSSP; P07996; 1LSL.
DR Genew; HGNC:18634; UNC5D.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL      1      32      Potential.
FT CHAIN       33     953     Netrin receptor UNC5D.
FT DOMAIN      33     379     Extracellular (Potential).
FT TRANSMEM    380    400     Potential.
FT DOMAIN      401    953     Cytoplasmic (Potential).
FT DOMAIN      54     151     Ig-like.
FT DOMAIN      153    244     Ig-like C2-type.
FT DOMAIN      252    306     TSP type-1 1.
FT DOMAIN      308    360     TSP type-1 2.
FT DOMAIN      540    642     ZU5.
FT DOMAIN      859    936     Death.
FT SITE        416    417     Cleavage (by caspase-3) (By similarity).
FT SITE        703    721     Interaction with DCC (By similarity).
FT DISULFID     75     134     By similarity.
FT DISULFID    180    231     By similarity.
FT CARBOHYD    117    117     N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD    228    228     N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD    353    353     N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD    376    376     N-linked (GlcNAc . . .) (Potential).
FT VARSPLIC     1      34     MGRAAATAGGGGGARRWLPWLGLCFWAAGTAAAR -> MIL
FT                                     VLVKALSDVCAGTSGFLLDFFSSQTSP (in isoform
FT                                     2).
FT                                     /FTId=VSP_011703.
SQ SEQUENCE    953 AA; 105879 MW; 5F893B9DF746F731 CRC64;

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Query Match 71.1%; Score 485; DB 1; Length 953;
 Best Local Similarity 66.7%; Pred. No. 2.2e-37;

Matches 78; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

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Qy      1 SASAAVIVYVNGGWSTWTEWSVCSASCGRGWQKRSRSCCTNPAPLNGGAFCEGQNVQKTAC 60
      | ||| :|||||||:|||| | : |||||:|||||:|||||:|||||:|||||
Db      242 SLSATVVVYVNGGWSSWTEWSACNVRCGRGWQKRSRTCTNPAPLNGGAFCEGMSVQKITC 301

Qy      61 ATLCVPDGSWSPWSKWSACGLDCTHWRSRECSDPAPRNGGEECQGTDLDTNCTSDL 117
      :||||||| ||:|| | :| | | |||: | ||||: |:|  :: ||| |
Db      302 TSLCPVDGSWEVWSEWSVCSPECEHLRIRECTAPPPRNGGKFCEGLSQESENCTDGL 358
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RESULT 12

UN5D_MOUSE

```
ID  UN5D_MOUSE      STANDARD;      PRT;      956 AA.
AC  Q8K1S2;
DT  25-OCT-2004 (Rel. 45, Created)
DT  25-OCT-2004 (Rel. 45, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4).
GN  Name=Unc5d; Synonyms=Unc5h4;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX  MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
RA  Engelkamp D.;
RT  "Cloning of three mouse Unc5 genes and their expression patterns at
RT  mid-gestation.";
RL  Mech. Dev. 118:191-197(2002).
CC  -!- FUNCTION: Receptor for netrin involved in cell migration. May be
CC  involved in axon guidance by mediating axon repulsion of neuronal
CC  growth cones in the developing nervous system upon ligand binding.
CC  Axon repulsion in growth cones may be caused by its association
CC  with DCC that may trigger signaling for repulsion. It also acts as
CC  a dependence receptor required for apoptosis induction when not
CC  associated with netrin ligand (By similarity).
CC  -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC  similarity).
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC  -!- TISSUE SPECIFICITY: Expressed in developing limb and mammary
CC  gland.
CC  -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC  similarity).
CC  -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC  cleavage does not take place when the receptor is associated with
CC  netrin ligand. Its cleavage by caspases is required to induce
CC  apoptosis (By similarity).
CC  -!- SIMILARITY: Belongs to the UNC-5 family.
CC  -!- SIMILARITY: Contains 1 death domain.
CC  -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC  -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC  -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC  -!- SIMILARITY: Contains 1 ZU5 domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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Db 240 SLSATVVVYVNGGWSSWTEWSACNVRGGRGWQKRSRTCTNPAPLNGGAFCEGMSVQKITC 299

Qy 61 ATLCVPDGSWSPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDRNCTSDL 117
 ||||| ||:| | :| | |||: | ||||: |:| :: || |

Db 300 TALCPVDGSWEVWSEWSVCSPECEHLRIRECTAPPPRNGGKFCEGLSQESENCTDGL 356

RESULT 13

UN5A_HUMAN

ID UN5A_HUMAN STANDARD; PRT; 842 AA.

AC Q6ZN44; Q8TF26; Q96GP4;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).

GN Name=UNC5A; Synonyms=KIAA1976, UNC5H1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX PubMed=14702039; DOI=10.1038/ngl285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,

RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,

RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,

RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,

RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

RT "Complete sequencing and characterization of 21,243 full-length human

RT cDNAs.";

RL Nat. Genet. 36:40-45(2004).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 302-842 FROM N.A.

RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 624-728 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21842142; PubMed=11853319;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXII.
 RT The complete sequences of 50 new cDNA clones which code for large
 RT proteins.";
 RL DNA Res. 8:319-327(2001).
 RN [4]
 RP INDUCTION.
 RX PubMed=12598906; DOI=10.1038/ncb943;
 RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
 RT "p53RDL1 regulates of p53-dependent apoptosis.";
 RL Nat. Cell Biol. 5:216-223(2003).
 RN [5]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones (By similarity).

CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q6ZN44-1; Sequence=Displayed;
 CC Note=No experimental confirmation available;
 CC Name=2;
 CC IsoId=Q6ZN44-2; Sequence=VSP_011694, VSP_011695;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q6ZN44-3; Sequence=VSP_011693;
 CC Note=No experimental confirmation available;
 CC -!- INDUCTION: By p53/TP53.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis (By similarity).
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues.
 CC Phosphorylated by PKC in vitro (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to the
 CC presence of introns.
 CC -----
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 CC -----
 DR EMBL; AK131380; BAD18531.1; -.
 DR EMBL; BC009333; AAH09333.2; -.
 DR EMBL; BC033727; -; NOT_ANNOTATED_CDS.
 DR EMBL; AB075856; BAB85562.1; ALT_SEQ.
 DR Genew; HGNC:12567; UNC5A.
 DR MIM; 607869; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 1.
 KW Alternative splicing; Apoptosis; Developmental protein;

KW Immunoglobulin domain; Phosphorylation; Receptor; Signal;
KW Transmembrane.

FT	SIGNAL	1	25	Potential.
FT	CHAIN	26	842	Netrin receptor UNC5A.
FT	DOMAIN	1	306	Extracellular (Potential).
FT	TRANSMEM	307	327	Potential.
FT	DOMAIN	328	842	Cytoplasmic (Potential).
FT	DOMAIN	44	141	Ig-like.
FT	DOMAIN	155	234	Ig-like C2-type.
FT	DOMAIN	242	294	TSP type-1.
FT	DOMAIN	439	542	ZU5.
FT	DOMAIN	761	841	Death.
FT	SITE	340	341	Cleavage (by caspase-3) (By similarity).
FT	SITE	605	623	Interaction with DCC (By similarity).
FT	DISULFID	65	124	By similarity.
FT	DISULFID	170	221	By similarity.
FT	CARBOHYD	107	107	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	218	218	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	287	287	N-linked (GlcNAc. . .) (Potential).
FT	VARSP LIC	1	97	MAVRPGLWLPALLGIVLAAWLRGSGAQQSATVANPVPGANPD
FT				LLPHFLVEPEDVYIVKNKPVLLVCKAVPATQIFFKCNGEWV
FT				RQVDHVIERSTDGSN -> MAGTSERSLISSISQPKAIECF
FT				EVKKKAFLTHGRYHGSGATPPKTKDPKPEFCGQT (in
FT				isoform 3).
FT				/FTId=VSP_011693.
FT	VARSP LIC	296	301	TASGPE -> SESSLP (in isoform 2).
FT				/FTId=VSP_011694.
FT	VARSP LIC	302	842	Missing (in isoform 2).
FT				/FTId=VSP_011695.
SQ	SEQUENCE	842 AA;	92958 MW;	3DFADCF973131849 CRC64;

Query Match 47.2%; Score 322; DB 1; Length 842;
Best Local Similarity 76.4%; Pred. No. 4.6e-22;
Matches 55; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

Qy 50 CEGQNV----QKTACATLCPVDGWSWPWSKWSACGLDCTHWSRECS DPAPRNGGEECQG 105
| :|: : :| : |||||
Db 221 CVAKNIVARRRSASAAVIVYVDGWSWPWSKWSACGLDCTHWSRECS DPAPRNGGEECQG 280

Qy 106 TDLDTRNCTSDL 117
|||||
Db 281 TDLDTRNCTSDL 292

RESULT 14

Q96SC3

ID Q96SC3 PRELIMINARY; PRT; 2673 AA.
AC Q96SC3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibulin-6 (Fragment).
GN Name=FIBL-6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RA Kostka G., Timpl R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ306906; CAC37630.1; -.
 DR HSSP; P07996; 1LSL.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000875; Cecropin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006605; G2F.
 DR InterPro; IPR009017; GFP_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR009138; Neural_cell_adh.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR Pfam; PF07645; EGF_CA; 8.
 DR Pfam; PF07474; G2F; 1.
 DR Pfam; PF00090; TSP_1; 6.
 DR PRINTS; PR01838; NCAMFAMILY.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00179; EGF_CA; 7.
 DR SMART; SM00408; IGc2; 17.
 DR SMART; SM00209; TSP1; 6.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS00268; CECROPIN; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50026; EGF_3; 5.
 DR PROSITE; PS01187; EGF_CA; 8.
 DR PROSITE; PS50835; IG_LIKE; 17.
 DR PROSITE; PS50092; TSP1; 6.
 KW EGF-like domain.
 FT NON TER 1 1
 SQ SEQUENCE 2673 AA; 291017 MW; BEAEC30B8340E272 CRC64;

Query Match 46.2%; Score 315; DB 2; Length 2673;
 Best Local Similarity 45.9%; Pred. No. 6.2e-21;
 Matches 51; Conservative 16; Mismatches 40; Indels 4; Gaps 2;

Qy 10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTAC-ATLCPVDG 68
 |:| || | | || |||:| | |:| || | ||:|:| | | ||| |
 Db 1680 VHGAWSAQWPWGTCSESCGKGTQTRARLCNNPPPAFGGSYCDGAETQMQVCNERNCVPVHG 1739
 Qy 69 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDRNCTSD 116
 |:|:| ||||:| | |:| |||| |:| |:|:|:|:|:| | ||
 Db 1740 KWATWASWSACSVSCGGGARQTRGCSDFVPQYGGRKCEGSDVQSDFCNSD 1790

RESULT 15
 Q69YJ3

ID Q69YJ3 PRELIMINARY; PRT; 1244 AA.
 AC Q69YJ3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFZp762L185 (Fragment).
 GN Name=DKFZp762L185;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RG The German cDNA Consortium;
 RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL833232; CAH10605.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006605; G2F.
 DR InterPro; IPR009017; GFP_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001491; Thrbomoduln.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR Pfam; PF00008; EGF; 3.
 DR Pfam; PF07645; EGF_CA; 7.
 DR Pfam; PF07474; G2F; 1.
 DR Pfam; PF00047; ig; 3.
 DR Pfam; PF00090; TSP_1; 6.
 DR PRINTS; PR00907; THRMBOMODULN.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00181; EGF; 7.
 DR SMART; SM00179; EGF_CA; 7.
 DR SMART; SM00682; G2F; 1.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00408; IGc2; 3.
 DR SMART; SM00209; TSP1; 6.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 7.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS50092; TSP1; 6.

KW EGF-like domain; Hypothetical protein.

FT NON_TER 1 1

SQ SEQUENCE 1244 AA; 136560 MW; 83C48651E9F3E238 CRC64;

Query Match 46.0%; Score 314; DB 2; Length 1244;

Best Local Similarity 45.0%; Pred. No. 3.8e-21;

Matches 50; Conservative 17; Mismatches 40; Indels 4; Gaps 2;

Qy 10 VNGGWSTWTEWSVCSASCGRGWQKRSRSCNTPAPLNGGAFCEGQNVQKTAC-ATLCPVDG 68

|:| || | | || |||:| | |:| || | ||::|:| | | ||:|

Db 368 VHGAWSAWQPWGTCSSESCGKGTQTRARLCNNPPPAFGGSYCDGAETQMVCNERNCPIHG 427

Qy 69 SWSPWSKWSACGLDC---THWRSRECSDPAPRNGGEECQGTDLDRNCTSD 116

|: |: ||| : | |:| ||| |: || |:|:|: : | ||

Db 428 KWATWASWSACSVSCGGGARQTRGCSDPVPQYGGRKCEGSDVQSDFCNSD 478

Search completed: March 1, 2005, 09:03:35

Job time : 21.4031 secs